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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 16:13:03 ; Search time 673 Seconds
(without alignments)
3494.414 Million cell updates/sec

Title: US-10-019-341-3

Perfect score: 2385

Sequence: 1 AQRDRFDIESKFAALRTE.....GRAPAVFKCHDKSLNKSG 448

Scoring table:

| | | |
|-------------|-------------|-------------|
| BLOSUM62 | Xgapop 10.0 | Xgapext 0.5 |
| Ygapop 10.0 | Ygapext 0.5 | |
| Fgapop 6.0 | Fgapext 7.0 | |
| Delop 6.0 | Delext 7.0 | |

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-Q=/cgn2.1/USPTO spo01/US10019341/runat 22102004_120137_1598/app query.fasta_1.647
-DB=N Geneseq 23Sep04 -QWT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPTXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10019341 @CGN 1 1 470 @runat 22102004_120137_1598 -NCPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N.Geneseq 23Sep04:.*
1: Geneseqn1980s:.*
2: Geneseqn1990s:.*
3: Geneseqn2000s:.*
4: Geneseqn2001as:.*
5: Geneseqn2001bs:.*
6: Geneseqn2002as:.*
7: Geneseqn2002bs:.*
8: Geneseqn2003as:.*
9: Geneseqn2003bs:.*
10: Geneseqn2003cs:.*
11: Geneseqn2003ds:.*
12: Geneseqn2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 2385 | 100.0 | 3549 | 2 | AAV41319 |
| 2 | 2385 | 100.0 | 3549 | 2 | AAV41319 Human lip |
| 3 | 2385 | 100.0 | 3549 | 6 | AAZ32183 Human lip |
| 4 | 2385 | 100.0 | 3549 | 6 | ABL66907 Lung canc |
| 5 | 2385 | 100.0 | 3549 | 6 | ABT10903 Human bre |
| 6 | 2385 | 100.0 | 3549 | 6 | ABT13006 Human lip |
| | | | | 12 | ADM41259 Human lip |

| | | | | | |
|----|--------|-------|------|----|----------|
| 7 | 2385 | 100.0 | 4314 | 12 | ADQ23742 |
| 8 | 2378 | 99.7 | 3635 | 9 | ACH03823 |
| 9 | 2372 | 99.5 | 4075 | 10 | ADB47407 |
| 10 | 2235.5 | 93.7 | 3617 | 10 | ADB58085 |
| 11 | 1996 | 83.7 | 1584 | 12 | ADP28939 |
| 12 | 1696 | 71.1 | 2939 | 2 | AAZ33576 |
| 13 | 1632.5 | 68.4 | 2933 | 2 | AAZ33576 |
| 14 | 1161 | 48.7 | 1503 | 6 | ABL91801 |
| 15 | 1161 | 48.7 | 1755 | 2 | AAZ33576 |
| 16 | 1161 | 48.7 | 2565 | 2 | AAZ33576 |
| 17 | 1161 | 48.7 | 2565 | 2 | AAZ33576 |
| 18 | 1161 | 48.7 | 2565 | 2 | AAZ33576 |
| 19 | 1161 | 48.7 | 2565 | 2 | AAZ33576 |
| 20 | 1161 | 48.7 | 2565 | 2 | AAZ33576 |
| 21 | 1161 | 48.7 | 2565 | 2 | AAZ33576 |
| 22 | 1161 | 48.7 | 2565 | 2 | AAZ33576 |
| 23 | 1161 | 48.7 | 2565 | 2 | AAZ33576 |
| 24 | 1158 | 48.6 | 1839 | 2 | AAZ33576 |
| 25 | 1158 | 48.6 | 1839 | 2 | AAZ33576 |
| 26 | 1157 | 48.5 | 3610 | 12 | ADP66756 |
| 27 | 1038 | 43.5 | 1603 | 6 | ABT13009 |
| 28 | 1038 | 43.5 | 1603 | 6 | ABT13009 |
| 29 | 1036 | 43.4 | 1553 | 10 | ADD29786 |
| 30 | 1019.5 | 42.7 | 1639 | 10 | ADC59370 |
| 31 | 1014.5 | 42.5 | 1605 | 6 | ABK63642 |
| 32 | 1014.5 | 42.5 | 1605 | 6 | ABK63642 |
| 33 | 962 | 40.3 | 1323 | 10 | ADP66756 |
| 34 | 962 | 40.3 | 1323 | 10 | ADP66756 |
| 35 | 928 | 38.9 | 1035 | 2 | AAV41621 |
| 36 | 928 | 38.9 | 1035 | 2 | AAV41621 |
| 37 | 928 | 38.9 | 1035 | 2 | AAV41621 |
| 38 | 928 | 38.9 | 1035 | 2 | AAV41621 |
| 39 | 928 | 38.9 | 1035 | 2 | AAV41621 |
| 40 | 928 | 38.9 | 1035 | 2 | AAV41621 |
| 41 | 928 | 38.9 | 1035 | 2 | AAV41621 |
| 42 | 928 | 38.9 | 1035 | 2 | AAV41621 |
| 43 | 928 | 38.9 | 1035 | 2 | AAV41621 |
| 44 | 928 | 38.9 | 1035 | 2 | AAV41621 |
| 45 | 928 | 38.9 | 1035 | 2 | AAV41621 |

ALIGNMENTS

RESULT 1

AAV41319
ID AAV41319 standard; DNA; 3549 BP.

XX AC AAV41319;

DT 09-NOV-1998 (first entry)

XX DE Human lipoprotein lipase gene.

XX DE Lipoprotein lipase; LPL gene; hypertension; exercise; human;

XX KW Lipoprotein lipase; LPL gene; hypertension; exercise; human;

XX KW Genetic marker; ss.

XX OS Homo sapiens.

XX FH Key

XX CDS Location/Qualifiers

FT sig_peptide

FT mat_peptide

XX PN WO9831835-A1.

XX PD 23-JUL-1998.

XX PF 22-DEC-1997; 97WO-US022974.

XX XX 16-JAN-1997; 97US-0035382P.

PR 27-MAY-1997; 97US-0048309P.
 XX (UYMA-) UNIV MARYLAND BALTIMORE.
 PA (UYPI-) UNIV PITTSBURGH.
 XX Hagberg JM, Ferrell RE;
 XX MPI; 1998-414128/35.
 DR P-PSDB; AAM68154.
 XX
 XX Analysis of genetic markers to identify subjects who will benefit from
 PT exercise - also assessing risk of cardiovascular disease from angiotensin
 PT -converting enzyme genotype.
 XX
 XX Disclosure; Page 29-32; 61pp; English.
 XX
 XX This is the human lipoprotein lipase (LPL) gene that encodes an enzyme
 CC (see AAM68154) that catalyzes the breakdown of triglycerides to release
 CC free fatty acids, and which may also be an important regulator of
 CC chylomicron metabolism. It is an object of the invention to identify
 CC individuals possessing a certain genotype and associated ailment, and to
 CC determine if the health of that individual can be improved by altering
 CC behavior. A claimed method comprises identifying individuals having a
 CC certain phenotype, determining the presence or absence of genetic markers
 CC associated with the phenotype, and instituting a lifestyle change to
 CC exploit or counteract the phenotype expressed by the gene marker. If the
 CC phenotype is hypertension, the gene marker is located at restriction
 CC sites (PvuII or HindIII) of the LPL gene locus and exercise training is
 CC instituted to decrease blood pressure. The gene marker can be identified
 CC by PCR amplification (see AAV41323-26) of the appropriate gene fragments.
 CC The general method can be used to identify subjects who will benefit most
 CC from physical exercise and also to identify those who are likely to be
 CC successful in sports
 XX
 XX Sequence 3549 BP; 1021 A; 741 C; 805 G; 982 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 4,046-237 Length: 3549
 Score: 2385.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-019-341-3 (1-448) x AAV41319 (1-3549)

QY 1 AlaAspGlnArgAspPheIleAspIleGluSerIlePheAlaLeuArgThrProGlu 20
 DB 256 GCCGACCAAGAGAGATTATTCGACATCGAAGTAATTTGCCCTTAGGACCCCTGAA 315
 QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
 DB 316 GACACAGCTGAGACACTTCCACCTCATTCGCCGAGTAGACAGTCCGTGGCTACCTGT 375
 QY 41 HisPheAsnHisSerSerIleThrPheMetValIleHisGlyThrValThrGlyMet 60
 DB 376 CAITTCATACACAGCAGCAAAACCTTCATGGTGATCCATCGCTGGACGGTAACAGGAATG 435
 QY 61 TyrGluSerTrpValProIleLeuValAlaAlaLeuTyrIleValAspSerAsn 80
 DB 436 TATGAGAGTGGGGCCAAACCTTGTGGCCGCCCTGTACAGAGAGAACCCAGACTCCCAAT 495
 QY 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
 DB 496 GTCAATTGGTGGACTGGCTGTCCGGCTCAGGAGCATTTACCCAGTGTCCGGGGGTAC 555
 QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluPheAsn 120
 DB 556 ACCAAACTGGTGGGACAGGATGTGGCCGGTTTATCAACTGGATGGAGGAGGATTTAAC 615
 QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyValAlaHisAlaAlaGlyIle 140
 DB 616 TACCCTCTGGACAAATGTCAATCTCTTGGATACAGCCCTTGGAGCCCATGCTGCTGGCATT 675

QY 141 AlaglySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
 DB 676 GCAGGAAGTCTGACCAATAGAAAGTCAACAGAAATTACTGCTCGATCCAGCTGGACCT 735
 QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
 DB 736 AACCTTTGAGTATGCAGAAAGCCCGAGTCTCTCTCTGATGATGAGATTTTGTAGAC 795
 QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
 DB 796 GTCTTACACACATTCCACAGAGGTCCCTGGTTCGAAGCATTTGGAATCCAGAACCCAGTT 855
 QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
 DB 856 GGGCATGTTGACATTTACCCGAATGGAGGTACTTTTCAGCCAGCATGTAAATTTGGAGAA 915
 QY 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
 DB 916 GCTATCCCGCTGATTCGACAGAGAGAGACTTGGCGATGTGGACCACTAGTGAAGTCTCC 975
 QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
 DB 976 CACGAGCCCTCCATTCATCTCTTCATCGACTCTCTGTTGAATGAAGAAATCCAAAGTAAG 1035
 QY 261 AlaTyrArgCysSerSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
 DB 1036 GCCTACAGGTGCAGTTCACGAGAGCCCTTCAGAAAGGCTCTGCTGAGTTGTAGAAG 1095
 QY 281 AsnArgCysAsnAsnLeuGlyTyrGluLeuAsnLysValArgAlaLysArgSerSerLys 300
 DB 1096 AACCCGCTGCAACAACTCTGGCTATGAGATCAATAAAGTCAGACCAAAAGAGACGACAAA 1155
 QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
 DB 1156 ATGTACTCTGAAGACTCGTTCTCAGATGCCCTCAAAAGTCTTCATTTACCAAGTAAAGATT 1215
 QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
 DB 1216 CATTTTCTGGGACTGAGAGTGAACCCCATACCAATCAGGCCTTTGAGATTTCTCTGTAT 1275
 QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
 DB 1276 GGCACCGTGGCGGAGAGTGAACAATCCCATTCACCTCGCTCGCTGAAAGTTTCCACAATAAG 1335
 QY 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeu 380
 DB 1336 ACCTACTCTCTCTTAATTTACACAGAGGTAGATATTGGAGAACTACTCATGTTTGAAGCTC 1395
 QY 381 LysTyrLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerSerProGlyPheAla 400
 DB 1396 AATGAGAGAGTGAATTCATCTTTAGCTGTGAGAGTGGTGGAGCAGTCCCGCTTGGCC 1455
 QY 401 IleGlnLysIleArgValLysAlaGlyGluThrGlnLysValIlePheCysSerArg 420
 DB 1456 ATTTCAGAAATCAGAGTAAAGAGGAGAGACTCAGAAAAGGTGATCTTCTGTCTAGG 1515
 QY 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
 DB 1516 GAGAAAGTGTCTCATTTTGCAGAAAGGAAAGGCACCTCGCGTATTGTGAAATGCCATGAC 1575
 QY 441 LysSerLeuAsnLysLysSerGly 448
 DB 1576 AAGTCTCTGAATAAGAAGTCAGGC 1599

RESULT 2
 AAZ32183
 ID AAZ32183 standard; cDNA; 3549 BP.
 XX
 XX AAZ32183;
 AC
 XX 13-JAN-2000 (first entry)
 DT
 XX

DE Human lipoprotein lipase nucleotide sequence.
 XX Human; coding sequence polymorphism; vascular pathology gene;
 KW polymorphic site; phenotype correlation; forensic; paternity testing;
 KW medicine; genetic analysis; vascular disease; ds.
 XX Homo sapiens.
 XX MO9950454-A2.
 PN 07-OCT-1999.
 XX
 XX 26-MAR-1999; 99MO-US0006473.
 XX
 XX 01-APR-1998; 98US-00054272.
 XX
 XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX Lander ES, Daley GQ, Cargill M, Ireland JS, Rozen SG;
 XX
 XX WPI; 1999-620066/53.
 DR P-PSDB; AAY49564.
 XX
 XX Determination of polymorphisms in genes, especially those identifying
 PT predisposition to vascular disease.
 XX
 XX Claim 1; Fig 27; 134pp; English.
 XX
 XX AAZ32159 to AAZ32194 represent reference alleles for specifically claimed
 CC nucleic acid sequences from the present invention which comprise
 CC polymorphic sites as given in a table in the specification, selected from
 CC 92 single nucleotide polymorphisms in which the nucleotide at the
 CC polymorphic site is different from a nucleotide at the same site in a
 CC reference allele. The nucleic acids, and primers and probes, are used to
 CC identify polymorphisms, which may predispose an individual to disease,
 CC especially a vascular disease. They can also be used in phenotype
 CC correlations, forensics, paternity testing, medicine or genetic analysis.
 CC AA49550 to AA49573 represent the proteins which correspond to some of
 CC the reference alleles
 XX
 SQ Sequence 3549 BP; 1020 A; 739 C; 806 G; 984 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. NO.: 4.04e-237 Length: 3549
 Score: 2385.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0
 US-10-019-341-3 (1-448) x AAZ32183 (1-3549)
 QY 1 AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
 Db 256 GCCGACCAAGAGAGATTTATCGACATCGAAGATAAATTTGCCCTAAGACCCCTGAA 315
 QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
 Db 316 GACACACCTGAGGACATCTGCCACCTCATTCGCCGAGTAGCAGAGTCCGTGGCTACCTGT 375
 QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTrpThrValThrGlyMet 60
 Db 376 CATTTCAATCACAGCAGCAAAACCTTCATGGTGATCATCGCTGAGCGGTACAGGANTG 435
 QY 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80
 Db 436 TATGAGAGTGGGTGGCCAAACCTTTGTGGCCGCCCTGTACAGAGAGAACCCAGACTCCAAAT 495
 QY 81 ValIleValIleAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
 Db 496 GTCAATGTGTGGTGGCTGTTCACGGGCTCAGAGCAATTACCAGTGTCCGGGGGTAC 555
 QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120

RESULT 3
 ABL66907

Db 556 ACCAAACTGGTGGGACAGGATGTGGCCGGTTTATCACTGGATGGAGGAGGATTTAAC 615
 QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaGlyIle 140
 Db 616 TACCTCTGGACAATGTCCATCTCTTGGGATACAGCCTTGGAGCCCATGCTGTGGCATT 675
 QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
 Db 676 GCAGGAAGTCTGACCAATAAGAAAGTCAACAGAAATTACTGGCCCTCGATCCAGCTGGACCT 735
 QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
 Db 736 AACTTTGAGTATGACAGAGCCCGAGTCTCTTCTCTGATGATGATGATGATGATGATGAT 795
 QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
 Db 796 GTCTTACACACATTCACAGAGGCTCCCTGGTGGAGCAATTGGAAATCCAGAAACCATGTT 855
 QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
 Db 856 GGGCATGTTGACATTTACCCGATGGAGGTACTTTTCAGCCAGGATGTAACTTGGAGAA 915
 QY 221 AlalleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
 Db 916 GCTATCCGCGTATTCAGAGAGAGGACTTGGAGATGTGGACCCAGCTAGTGAAGTCTCTC 975
 QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
 Db 976 CACGAGCGCTCATTCATCTCTTCATCGACTCTCTGTTGAATGAAGAAATCAAGTAAG 1035
 QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
 Db 1036 GCTACAGCTGCAGTCTCCAGGAGCCCTTGGAAAGGCGCTCTGCTTGAAGTTGTGAAGAAG 1095
 QY 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerLys 300
 Db 1096 AACCGCTGCAACAATCTGGGCTATGAGATCAATAAAGTCAGAGCCAAAGAGACGACAA 1155
 QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
 Db 1156 ATGTACCTGAAGACTCGTTCTCAGATGCCCTACAAAGCTTCCATTACCAAGTAAGATT 1215
 QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
 Db 1216 CATTTTCTGGGACTGAGAGTGAAACCCATACCAATCAGGCTTTCAGATTTCTCTGAT 1275
 QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
 Db 1276 GGCACCGTGGCCGAGAGTGAGAACATCCCATTCATCTGCTGAAGTTTCACAAATTAAG 1335
 QY 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeu 380
 Db 1336 ACCTACTCTCTTCTTAATTTACAGAGGTAGATTTGGAGAACTACTCATGTTGAAGCTC 1395
 QY 381 LysTrpLysSerAspSerTyrPheSerTyrPheSerTrpTrpSerSerProGlyPheAla 400
 Db 1396 AAATGGAAGAGTGATTCATCTTACTTGTGTGAGCTGTGGAGAGCTCCCGGCTTCGCC 1455
 QY 401 IleGlnIleValIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
 Db 1456 ATTCAAGATCATGAGTAAAGAGCAGAGACTCAGAAAAAGGTGATCTTCTGTTCTAGG 1515
 QY 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
 Db 1516 GAGAAAGTGTCTCATTTGGAGAAAGGAAAGGCCCTCGCGTATTTGTGAAATGCCATGAC 1575
 QY 441 LysSerLeuAsnLysLysSerGly 448
 Db 1576 AAGTCTCTGAATAAGAGTCAGGC 1599

Mon Oct 25 15:42:52 2004

us-10-019-341-3.rng

ABL66907 standard; DNA; 3549 BP.

ABL66907;

15-MAY-2002 (first entry)

Lung cancer related gene sequence SEQ ID NO:5244.

Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytosaratic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma; gene; ds.

Homo sapiens.

WO200194629-A2.

13-DEC-2001.

30-MAY-2001; 2001WO-US010838.

05-JUN-2000; 2000US-0209473P.

05-JUN-2000; 2000US-0209531P.

18-SEP-2000; 2000US-0233133P.

20-SEP-2000; 2000US-0233617P.

20-SEP-2000; 2000US-0234009P.

20-SEP-2000; 2000US-0234034P.

22-SEP-2000; 2000US-0234052P.

22-SEP-2000; 2000US-0234509P.

22-SEP-2000; 2000US-0234567P.

25-SEP-2000; 2000US-0234923P.

25-SEP-2000; 2000US-0234924P.

25-SEP-2000; 2000US-0235077P.

25-SEP-2000; 2000US-0235082P.

25-SEP-2000; 2000US-0235134P.

25-SEP-2000; 2000US-0235280P.

26-SEP-2000; 2000US-0235637P.

26-SEP-2000; 2000US-0235638P.

27-SEP-2000; 2000US-0235711P.

27-SEP-2000; 2000US-0235720P.

27-SEP-2000; 2000US-0235840P.

27-SEP-2000; 2000US-0235863P.

28-SEP-2000; 2000US-0236028P.

28-SEP-2000; 2000US-0236032P.

28-SEP-2000; 2000US-0236033P.

28-SEP-2000; 2000US-0236034P.

28-SEP-2000; 2000US-0236109P.

28-SEP-2000; 2000US-0236111P.

29-SEP-2000; 2000US-0236842P.

29-SEP-2000; 2000US-0236891P.

02-OCT-2000; 2000US-0237172P.

02-OCT-2000; 2000US-0237278P.

02-OCT-2000; 2000US-0237294P.

02-OCT-2000; 2000US-0237295P.

02-OCT-2000; 2000US-0237316P.

03-OCT-2000; 2000US-0237425P.

03-OCT-2000; 2000US-0237598P.

03-OCT-2000; 2000US-0237604P.

03-OCT-2000; 2000US-0237606P.

03-OCT-2000; 2000US-0237608P.

01-NOV-2000; 2000US-0244867P.

01-NOV-2000; 2000US-0245084P.

(AVAL-) AVALON PHARM.

Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;

Soppet DR, Weaver Z;

WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change

in expression of a gene of a signature gene set.

Claim 1; SEQ ID NO 5244; 44pp; English.

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour

Sequence 3549 BP; 1020 A; 739 C; 806 G; 984 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,04e-237 Length: 3549
Score: 2385.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-019-341-3 (1-448) x ABL66907 (1-3549)

| | | | |
|----|-----|--|-----|
| QY | 1 | AlaAspGlnArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu | 20 |
| DB | 256 | GCAGCAACCAAGAGAGATTTTATCGACATCGAAGATTAATTTCCCTAGGACCCCTGAA | 315 |
| QY | 21 | AspThrAlaGluAspThrCysHisLeuLeuProGlyValAlaGluSerValAlaThrCys | 40 |
| DB | 316 | GACACAGCTGAGACACTGCGCCCTCATTCGCGAGTAGCAGAGTCGCTGCTGCTGT | 375 |
| QY | 41 | HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTrpThrValThrGlyMet | 60 |
| DB | 376 | CATTTCATCATCAGCAGCAAAACCTTCATGCTGATCCATGCTGGAGCGGTAACAGGAATG | 435 |
| QY | 61 | TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn | 80 |
| DB | 436 | TATGAGAGTTGGTGCCAAACCTTGTCGCGCCCTGTACAGAGAGAACAGACTCCAAT | 495 |
| QY | 81 | ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr | 100 |
| DB | 496 | GTCTTTGTGTGACCTGGCTGTGTCACGGGCTCAGAGACATTTACCCAGTGTCCGGGGTAC | 555 |
| QY | 101 | ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn | 120 |
| DB | 556 | ACCAAACTGCTGGACAGGATGTGGCCCGCTTTATCACTGGATGGAGGAGGAGTTAAC | 615 |
| QY | 121 | TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyIle | 140 |
| DB | 616 | TACCCCTCTGGACCAATGTCCATCTCTTGGGATACAGCCTTGAGCCCATGCTGTGGCAT | 675 |
| QY | 141 | AlaGlySerLeuThrAsnLysValAsnArgIleThrGlyLeuAspProAlaGlyPro | 160 |
| DB | 676 | GCAGGAGTCTGACCAATAGAAAGTCAACAGAAATTTACTGGCTCGATCCAGCTGGACCT | 735 |
| QY | 161 | AspPheGluTyrAlaGluAlaProSerArgLeuSerProAspAlaAspPheValAsp | 180 |
| DB | 736 | AACCTTGAGTATGAGAAGCCCGAGTCGTCTTCTCTGATGATGAGATTTTGTAGAC | 795 |
| QY | 181 | ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal | 200 |
| DB | 796 | GTCTTACACATTCACAGAGGGTCCCTGCTGAGGAGCATTTGGATCCAGAACCACTT | 855 |

QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
 Db 856 GGGCATGTTGACATTTACCCGATGAGGAGTACITTTTCAGCCAGGATGATCAATGGAGAA 915
 QY 221 AlaileArgValIleAlaGluArgGlyVleuGlyAspValAspGlnLeuValCysCysSer 240
 Db 916 GCTATCCGCTGATTTGAGAGAGAGGACTTTGGAGATGTGACAGCTAGTGAAGTGTCC 975
 QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGlnGluAsnProSerLys 260
 Db 976 CACGAGCGCTCCATTCATCTCTTCATCGACTCTCTGTGTAATGAAGAAATCCAAAGTAAG 1035
 QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
 Db 1036 GCTACAGGTGCAGTTCCTCAAGGAAGCTTTGAGAAAGGCTCTGCTTGATTTGTAAGAG 1095
 QY 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerLys 300
 Db 1096 AACCGCTGCACAAATCTGGCTATGAGATCAATAAAGTCAGAGCCAAAGAGACGACAAA 1155
 QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
 Db 1156 ATGTACTCTGAAGACTGTTCTCAGATGCCCTCAAAAGTCTTCCATTACCAAGTAAAGATT 1215
 QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
 Db 1216 CATTTTCTGGAGCTGAGAGTGAACCCCAATACCAATCAGCCCTTTGAGATTCTCTGAT 1275
 QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
 Db 1276 GGCACCGTGGCGAGAGTGAGAACATCCCATCTGCTGGAAGTTTCACAAATAAG 1335
 QY 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuMetLeuLysLeu 380
 Db 1336 ACCTACTCTCTCTTAATTTACAGAGAGTATGATTTGGAGAACTACTCATGTGTAAGTC 1395
 QY 381 LysTyrLysSerAspSerTyrPheSerTyrPheSerTyrPheSerProGlyPheAla 400
 Db 1396 AAATGGAGAGATGATTCATCTTTAGCTGGTCAGACTGGTGAGCAGTCCCGGCTTCGCC 1455
 QY 401 IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
 Db 1456 ATTCAAGAGATCAGAGTAAAGCAGGAGAGACTCAGAAAAGGTGATCTTCTGTCTAGG 1515
 QY 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
 Db 1516 GAGAAAGTGCTCATTTTGCAGAAAGGAAGGACCTCGGGTATTTGTGAAATGCCATGAC 1575
 QY 441 LysSerLeuAsnLysLysSerGly 448
 Db 1576 AAGTCTCTGAATAAGAGTCAGGC 1599

RESULT 4

ABT10903
 ID ABT10903 standard; cDNA; 3549 BP.
 XX AC ABT10903;
 XX DT
 XX DE
 XX OS Human breast cancer associated coding sequence SEQ ID NO: 1037.
 XX KW Human; breast specific gene; breast cancer; differential expression;
 XX KW cytosolic; gene therapy; gene; ss.
 XX OS Homo sapiens.
 XX PN WO200259271-A2.
 XX PD
 XX XX 01-AUG-2002.
 XX PF 25-JAN-2002; 2002WO-US002176..

XX PR 25-JAN-2001; 2001US-0263757P.
 PR 25-APR-2001; 2001US-0286090P.
 PR 23-MAY-2001; 2001US-0292517P.
 XX PA (GENE-) GENE LOGIC INC.
 XX PI Orr MS, Nation M, Diggins JC, Zeng W;
 XX WIPI; 2002-674803/72.
 XX PT Diagnosing breast cancer in a patient comprises detecting the level of
 PT gene expression in cell or tissue samples, where a differential gene
 PT expression is indicative of breast cancer.
 XX PS Claim 1; SEQ ID NO 1037; 260pp + Sequence Listing; English.
 XX CC The present invention relates to methods of diagnosing breast cancer in a
 CC patient, which comprise detecting the level of expression in a tissue
 CC sample of two or more genes selected from those shown in ABT09867-
 CC ABT1112, where a differential expression of the genes indicates breast
 CC cancer. The methods are useful in diagnosing, treating, detecting the
 CC progression, and in monitoring treatment of breast cancer in patients.
 CC The methods are also useful as a screening tool for agents that modulate
 CC the onset or progression of breast cancer. The breast cancer genes may be
 CC used as diagnostic markers for the prediction or identification of the
 CC malignant state of breast tissue, for confirming the type and progression
 CC of cancer, and for drug screening and assays. The present sequence is a
 CC coding sequence of the invention. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub.published_pct_sequences
 XX SQ Sequence 3549 BP; 1020 A; 739 C; 806 G; 984 T; 0 U; 0 Other;

Alignment Scores:

| Pred. No.: | 4.04e-237 | Length: | 3549 |
|------------------------|-----------|---------------|------|
| Score: | 2385.00 | Matches: | 448 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |

US-10-019-341-3 (1-448) x ABT10903 (1-3549)

| QY | 1 | AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu | 20 |
|----|-----|---|-----|
| Db | 256 | GCCGACCAAGAGAGATTTTATCGACATCGAAAGTAAATTTGCCCTTAAGGACCCCTGAA | 315 |
| QY | 21 | AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys | 40 |
| Db | 316 | GACACAGCTGAGGACACTTGCACCTCATTTCCGGAGTAGCAGAGTCCGCTGCTTACTGT | 375 |
| QY | 41 | HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTyrThrValThrGlyMet | 60 |
| Db | 376 | CATTTCATACAGCAGCAAACTTCATGTCATCATCGCTGACGGTAAACAGGATG | 435 |
| QY | 61 | TyrGluSerTyrValProLysLeuValAlaLeuTyrLysArgGluProAspSerAsn | 80 |
| Db | 436 | TATGAGATGGGTGCCAAACTTGTGGCGCCCTGTACAAGAGAGAACACAGACTCCAAT | 495 |
| QY | 81 | ValIleValValAspTyrPheLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr | 100 |
| Db | 496 | GTCAATGTGTGGACTGGTGTGTCACGGGTCTAGGACCATTACCCAGTGTCCGCGGTAC | 555 |
| QY | 101 | ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTyrMetGluGluPheAsn | 120 |
| Db | 556 | ACCAAACTGGTGGGACAGGATGTGGCCCGGTTTATCACTGGATGGAGGAGGATTAAAC | 615 |
| QY | 121 | TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaGlyIle | 140 |
| Db | 616 | TACCTCTGGCAATGTCCATCTCTTGGGATACAGCCTTGGAGCCCATCTGCTGTCATT | 675 |

PT /*tag= v
 XX /note= "Single nucleotide polymorphism"

PN WO200272604-A2.

PD 19-SEP-2002.

PF 05-MAR-2002; 2002WO-US006728.

PR 09-MAR-2001; 2001US-00802640.

XX (SEQU-) SEQUENOM INC.

XX Braun A, Bansal A, Kleya PW;

XX WPI; 2002-750478/81.

DR P-PSDB; AA015884.

XX
 PT Detecting the presence or absence of an allelic variant of a polymorphic
 PT region of COX6B and/or GPI-1 gene, useful for detecting a predisposition
 PT to high serum cholesterol, low serum HDL and cardiovascular disease.
 XX
 PS Disclosure; Page 111-113; 199pp; English.

XX
 CC The invention comprises methods of detecting the presence or absence of
 CC at least one allelic variant of a polymorphic region of a gene associated
 CC with cardiovascular disease. The invention specifically relates to
 CC detecting the region of a cytochrome C oxidase subunit VIB (COX6B) gene
 CC that is associated with high serum cholesterol, or the region of the N-
 CC acetylglucosaminyl transferase component glycosylphosphatidylinositol-1
 CC (GPI-1) gene that is associated with low serum high density lipoprotein
 CC (HDL). The methods of the invention are useful for detecting a
 CC predisposition to high serum cholesterol, low serum HDL and
 CC cardiovascular disease. The methods are also useful for elucidating
 CC pathological pathways, developing diagnostic assays and new drug
 CC therapies for such disorders. The present DNA sequence represents a human
 CC gene associated with high serum cholesterol, low serum HDL and/or
 CC cardiovascular disease

SQ Sequence 3549 BP; 1020 A; 739 C; 806 G; 984 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.04e-237 Length: 3549
 Score: 2385.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-019-341-3 (1-448) x ABT13006 (1-3549)

QY 1 AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
 Db 256 GCCGACCAAGACAGAGATTATTCGACATCGAAAGTAAATTTGCCCTTAAGACCCCTGAA 315
 QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
 Db 316 GACACAGCTCAGGACACTGCCACCTCATTCGCCGAGTAGCAGATCCGGTGGCTTACCTGT 375
 QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTrpThrValThrGlyMet 60
 Db 376 CATTTCAATCAGACGACGACAAACCTTCATGGTATCCATGGCTGGACGGTAACAGGAATG 435
 QY 61 TyrGluSerTrpValProLysLeuValAlaLeuTyrLysArgGluProAspSerAsn 80
 Db 436 TATGAGAGTTGGTGGCAAACTTTGGCCGCCCTGTACAAAGAGAGAACACAGACTCCAAT 495
 QY 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
 Db 496 GTCAATGTGTGGACTGGCTGTCAACGGCTCAGAGCAATACCAATGTCGGGGGCTAC 555
 QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120

Db 556 ACCAACTGTGGGACAGGATGTGGCCCGGTTTATCACTGGATGGAGGAGGTTTAAAC 615
 QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyTle 140
 Db 616 TACCTCTGGACCAATGTCCATCTCTTGGGATACAGCCCTTGGAGCCCATGTCTGGCATT 675
 QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
 Db 676 GCAGGAAGTCTGACCAATTAAGAAAGTCAACAGAAATTACTGGCCCTCGATCCAGCTGGACCT 735
 QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
 Db 736 AACTTTGAGTATGCAGAAGCCCGAGTCTCTTCTCTGATGATGCAGATTGTAGAC 795
 QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
 Db 796 GTCTTACACACATTCCACAGAGGTCCTCTGGTGGAAAGCAATTGGAAATCCAGAAACAGATT 855
 QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
 Db 856 GGGCATGTGACATTTACCCGAATGGAGGTACTTTTCAGCCAGGATGTAACTTGGAGAA 915
 QY 221 AlalleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
 Db 916 GCTATCCGCGTGAATTCAGAGAGAGGACTTGGAGATGTGGACAGCTAGTGAAGTCTCC 975
 QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
 Db 976 CACGAGCGCTCCATTCATCTCTTCATGACTCTCTGTGTAATGAAGAAATCAAGTAAG 1035
 QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
 Db 1036 GCCTACAGGTGCAGTTCCAGGAAGCCTTTGAGAAAGGCTCTGCTTGAGTTGTAGAAG 1095
 QY 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValaArgAlaLysArgSerLys 300
 Db 1096 AACCGCTGCAACAATCTGGGCTATGAGATCAATAAAGTCAGAGCCAAAGAACAGCAAA 1155
 QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
 Db 1156 ATGTACCTGAAGACTCGTTCTCAGATGCCCTACAAAGTCTTCCATTACCAAGTAAAGATT 1215
 QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
 Db 1216 CATTTTCTGGACTGAGAGTGAAACCCATACCAATCAGGCTTTGAGATTCTCTGTAT 1275
 QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
 Db 1276 GGCACCCGTGGCCGAGAGTGAGAACATCCCATTCATCTGCTGAAGTTTCCACAAATAG 1335
 QY 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeu 380
 Db 1336 ACCTACTCTCTCTTAATTTACAGAGGTAGATTATTGGAGAACTACTCATGTTGAAGCTC 1395
 QY 381 LysTrpLysSerAspSerTyrPheSerTyrPheSerTyrPheSerTyrPheSerTyrPhe 400
 Db 1396 AAATGGAAGAGTGATTCATCTTACTGTGTGAGCTGTGGAGCAGTCCCGGCTTCGCC 1455
 QY 401 IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
 Db 1456 ATTCAAGAGATCAGAGTAAAGCAGGAGAGACTCAGAAAAAGGTGATCTTCTGTCTAGG 1515
 QY 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
 Db 1516 GAGAAAGTCTCTCATTTTGCAGAAAGAAAGGACCTGCGGTATTTGTGAAATCCCATGAC 1575
 QY 441 LysSerLeuAsnLysLysSerGly 448
 Db 1576 AAGTCTCTGAATAAGAAAGTCAGGC 1599

RESULT 6
 ADM41259
 ID ADM41259 standard; DNA; 3549 BP.

ADM41259;
03-JUN-2004 (first entry)
Human lipoprotein lipase gene.
Liver X receptor; lipoprotein lipase; antiatherosclerotic; nootropic;
neuroprotective; litholytic; hepatotropic; antidiabetic; anorectic;
antiinflammatory; 4-oxo-quinazoline; agonist; human; gene; enzyme; ds.
Homo sapiens.
EP1398032-A1.
17-MAR-2004.
10-SEP-2003; 2003EP-00020417.
10-SEP-2002; 2002EP-00020255.
(PHEN-) PHENEX PHARM AG.
Kober I, Albers M, Koegl M, Blume B, Deuschle U, Kremoser C;
WPI: 2004-259060/25.
GENBANK; M15856.
Novel 4-oxo-quinazoline compound useful for treating atherosclerosis,
Alzheimers disease, gallstone disease, Type II diabetes, lipid disorders,
obesity, inflammatory or cardiovascular disorder.
Dislosure; SEQ ID NO 15; 85pp; English.
The present sequence is that of the human lipoprotein lipase (LPL) gene.
This is an example of a gene that is regulated through binding of a liver
X receptor (LXR) agonist to the LXR protein. The invention relates to 4-
oxo-quinazolines which bind to LXR alpha or LXR beta, acting as selective
agonists of the receptor. Such compounds are useful for treating a
disease which is affected by cholesterol, triglyceride, bile acid,
glucose or glucocorticoid levels in a mammal (especially a human). They
can be used for the prevention or treatment of mammalian atherosclerosis,
gallstone disease, lipid disorders, type 2 diabetes, Alzheimer's disease,
skin disorders, inflammation, obesity or cardiovascular disorders such as
coronary heart disease or stroke. The compounds can be used to block a
cholesterol absorption in a mammal, to treat obesity and to modulate a
gene whose expression is regulated by LXR alpha or LXR beta (claimed).
Expression of LPL is increased upon administration of a compound of the
invention.
XX
SQ Sequence 3549 BP; 1020 A; 739 C; 806 G; 984 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 4.04e-237 Length: 3549
Score: 2385.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-10-019-341-3 (1-448) x ADM41259 (1-3549)
QY 1 AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
Db 256 GCGCACCAAGAAGAGATTATTATCGACATCGAAGTAATTTGGCTTAAGGACCCCTGAA 315
QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
Db 316 GACACAGCTGAGGACACTTGGCCACCTCATTCGCGAGTAGCAGAGTCCGTCGTACCTGT 375
QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTyrThrValThrGlyMet 60
Db 376 CATTTCAATCATCAGCAGCAAAACCTTCATGGTGATCCATGGCTGACGCGGTACAGGAATG 435

QY 421 GluLysValSerHisLeuGlnLysGlyAlaProAlaValPheValLysCysHisAsp 440
 Db 1516 GAGAAAGTGCTCATTTGACAGAAAGGACACCTCGGTATTTGTAATGCCATGAC 1575
 QY 441 LysSerLeuAsnLysLysSerGly 448
 Db 1576 AAGTCTCTGAATAAGAGTCAGGC 1599

RESULT 7

ADQ23742

ID ADQ23742 standard; DNA; 4314 BP.

AC ADQ23742;

XX ADQ23742;

XX 26-AUG-2004 (first entry)

XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 6562.

XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
 KW ds.

XX Homo sapiens.

XX WO2004048938-A2.

XX 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US038193.

XX 26-NOV-2002; 2002US-0429739P.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Aziz N, Ginsburg WM, Zlotnik A;

XX WPI; 2004-441208/41.

XX Early detection of soft tissue sarcoma comprises determining expression

XX of a gene in a first soft tissue sample and a normal soft tissue sample

XX and comparing the gene expression, also useful in treating soft tissue

XX sarcoma.

XX Example 2; SEQ ID NO 6562; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma

XX which comprises obtaining a first soft tissue sample from an individual

XX and a normal soft tissue sample from the same or different individual,

XX determining the expression of a gene in both samples and comparing the

XX expression of the gene in both soft tissue samples, where a higher level

XX of protein expression in the first soft tissue sample indicates the

XX presence of soft tissue sarcoma. The method of the invention has

XX cytotostatic applications and may be useful for detecting soft tissue

XX sarcoma, possibly via gene therapy or vaccine production. The nucleic

XX acid sequences may be useful in diagnostic and screening applications.

XX The current sequence is that of a human soft tissue sarcoma-upregulated

XX DNA of the invention. The current sequence is not shown within the

XX specification per se but was submitted in CD format by the inventor.

XX SQ Sequence 4314 BP; 1314 A; 895 C; 981 G; 1124 T; 0 U; 0 Other;

XX Alignment Scores:

XX Pred. No.: 5,41e-237 Length: 4314

XX Score: 2385.00 Matches: 448

XX Percent Similarity: 100.00% Conservative: 0

XX Best Local Similarity: 100.00% Mismatches: 0

XX Query Match: 100.00% Indels: 0

XX DB: 12 Gaps: 0

XX US-10-019-341-3 (1-448) x ADQ23742 (1-4314)

QY 1 AlaAspGlnArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20

Db 750 GCCGACCAAGAGAGATTATTCGACATCGAAAGTAAATTTGCCCTAAGACCCCTGAA 809

QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
 Db 810 GACACAGCTGAGGACACTTCCACCTCATTTCCCGAGTAGCAGAGTCCGTGGCTACCTGT 869
 QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyThrThrValThrGlyMet 60
 Db 870 CATTTCAATCACAGCAGCAAAACCTTCATGGTGATCCATGGCTGGACGGTAACAGGATG 929
 QY 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80
 Db 930 TATGAGAGTTGGTGCCAAACTTGTGGCGCCCTGTACAAGAGAGAACAGACTCCAAT 989
 QY 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
 Db 990 GTCAATTTGGTGACTGGCTGTACCGGGTCTAGGAGCATTTACCACTGTCCGGGCTAC 1049
 QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120
 Db 1050 ACCAACTGGTGGACAGGATGTGGCCGGTTTATCAACTGGATGGAGGAGGATTAAC 1109
 QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaGlyIle 140
 Db 1110 TACCTCTGGACATGTCCATCTCTGGGATACAGCTTTGGAGCCCATCTGTGGCAAT 1169
 QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
 Db 1170 GCAGGAAGTCTGACCAATAAGAAAGTCAACAGAAATTTACTGGCTCGATCCAGCTGGACT 1229
 QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAlaAspPheValAsp 180
 Db 1230 AACTTTGAGTATGCAGAAAGCCCGAGTCTCTTCTCTGATGATGCAGATTTGTAGAC 1289
 QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
 Db 1290 GTCTTACACATTCACCAGAGGGTCCCTCGTGAAGCATTTGGAATCCAGAAACAGTT 1349
 QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
 Db 1350 GGGCATGTGACATTTACCCGAATGGAGTACTTTTCAGCCAGGATGTAACATTTGGAGAA 1409
 QY 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
 Db 1410 GCTATCCCGTGATGTCAGAGAGAGACTTGGAGATGTGGACCACTAGTAGTGAAGTCTCC 1469
 QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
 Db 1470 CACGAGCGCTCCATTCATCTCTTCATCGACTCTCTGTGAATGAAGAAATCCAAAGTAAG 1529
 QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
 Db 1530 GCCTACAGGTGCACTTCCNAGGAGCCCTTGAGNAGGGCTCTCTGTGAGTTGTAGAAAG 1589
 QY 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys 300
 Db 1590 AACCGCTGCAACAATCTGGGCTATGAGATCAATAAAGTCAGAGCCAAAGAGACGACAA 1649
 QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
 Db 1650 ATGTACTGAAGACTCGTTCTCAGATGCCCTACAAAGTCTTCCATTTACCAAGTAAGATT 1709
 QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
 Db 1710 CATTTTCTGGGACTGAGAGTGAACCCATACCAATCAGGCCTTTGAGATTTCTCTGTAT 1769
 QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
 Db 1770 GGCACCGTGGCGGAGAGTGAACAATCCCATTCACCTCGCTCGCTGAAGATTCCCAAAATAG 1829
 QY 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeu 380
 Db 1830 ACTTACTCTCTTAATTTACACAGAGGTAGATATTGGAGAACTACTCATGTGTGAAGCTC 1889

Mon Oct 25 15:42:52 2004

381 LysTrpLysSerAspSerTrpPheSerTrpSerAspTrpTrpSerSerProGlyPheAla 400
 1890 AATGGAGAGTGTATTCATCTAGTCTGTGAGACTGGTGGAGAGTCCCGGCTCGCC 1949
 401 IleGlnLysLysArgValLysAlaGlyGluThrGlnLysLysValLysPheCysSerArg 420
 1950 ATTGAGAGATCAGAGTAAAGCAGGAGAGACTCAGAAAAGGTGATCTTCTGTTCTAGG 2009
 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
 2010 GAGAAAGTGTCTATTGTCAGAAAGGAAAGCAGCTGCGGTATTGTAATGCAATGATC 2069
 441 LysSerLeuAsnLysLysSerGly 448
 2070 AAGTCTCTGTAATAAGAGTCAAGC 2093

RESULT 8
 ACH03823
 ID ACH03823 standard; cDNA; 3635 BP.
 XX ACH03823;
 AC ACH03823;
 XX 26-SEP-2003 (first entry)
 DT Human cDNA differentially expressed in lung cancer #28.
 DE Gene therapy; emphysema; ss; gene; chronic obstructive pulmonary disease;
 KW respiratory disorder; lung cancer; asthma; human.
 XX Homo sapiens.
 OS US2003065157-A1.
 XX US2003065157-A1.
 XX 03-APR-2003.
 PD 04-APR-2002; 2002US-00116802.
 XX 04-APR-2001; 2001US-0281593P.
 PR (LASEK A W.
 PA Lasek AW;
 XX WPI; 2003-540803/51.
 XX New combination comprising cDNAs that are differentially expressed in
 PT respiratory disorders, useful for diagnosing or treating respiratory
 PT disorders e.g., lung cancer, chronic obstructive pulmonary disease,
 PT emphysema or asthma.
 XX Claim 1; Page; 39pp; English.
 XX The invention relates to a combination comprising cDNAs or their
 CC complements that are differentially expressed in respiratory disorder.
 CC The combination is useful for preparing a composition for diagnosing or
 CC treating respiratory disorders e.g. lung cancer, chronic obstructive
 CC pulmonary disease, emphysema or asthma. The present sequence represents
 CC human cDNA differentially expressed during lung cancer
 XX Sequence 3635 BP; 1053 A; 752 C; 824 G; 1006 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,24e-236 Length: 3635
 Score: 2378.00 Matches: 447
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.78% Mismatches: 0
 Query Match: 99.71% Indels: 0
 DB: 9 Gaps: 0
 US-10-019-341-3 (1-448) x ACH03823 (1-3635)

1 AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20

331 GCCGACCAAGAGAGATTTTATCGACATCGAAGTAAATTTGCCCTAAGGACCCCTGAA 390
 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
 391 GACACAGCTGAGGACACTTCCACCTCATTTCCCGAGTAGCAGAGTCCGTGGCTACCTGT 450
 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyThrPheValThrGlyMet 60
 451 CATTTCAATCACAGCAGCAAAACCTTCATGGTGATCAATGGCTGAGCGTAAACAGGAATG 510
 61 TyrGluSerTrpValProLysLeuValAlaLeuTyrLysArgGluProAspSerAsn 80
 511 TATCAGAGTTGGGTGCCAAAACCTTGTGGCCGCTGTACAGAGAGAACAGAGATCCCAAT 570
 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
 571 GTCATTGTGGTGGACTGGCTGTACGGCTCAGAGCATTTACCCAGTGTCCCGGGCTAC 630
 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120
 631 ACCAACTGGTGGGACAGATGTGGCCCGGTTTATCAACTGGATGGAGGAGGAATTTAAC 690
 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyValAlaAlaGlyIle 140
 691 TACCTCTGGCAATGTCCATCTCTGGGATACAGCTTGGAGCCCATGCTGCTGGCAT 750
 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
 751 GCGGAAGTCTGACCAATAGAAAGTCAACAGATTTACTGGCTCGATCCAGCTGGACCT 810
 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
 811 AACTTTGAGTATGCAGAGCCCGAGTGTCTTCTCTCTGATGATGCAGATTTGTAGAC 870
 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
 871 GTCTTACACACATTCACAGAGGGTCCCTGTGTGGAAGCATTTGGAATCCAGAAACAGTT 930
 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
 931 GGGCATGTTGACATTTTACCCGATGGAGTACTTTTACCCAGGATGTAACTTGGAGAA 990
 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
 991 GCTATCCGCGTGTATTCAGAGAGAGACTTGGAGATGTGACAGCTAGTGAAGTGTCTCC 1050
 241 HisGluArgSerIleHisPheIleAsnSerLeuLeuAsnGluGluAsnProSerLys 260
 1051 CACGAGCGTCCATTCATCTTTCATCGACTCTCTGTGTAATGAGAAATCCAGTAAG 1110
 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
 1111 GCCTACAGGTGCAGTTCCAAAGGAGGCTTTGAGAAAGGGCTCTGCTGATGTAGAAAG 1170
 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys 300
 1171 AACCGTGCACCAATCTGGCTATGAGATCAATAAAGTCAAGCCCAAGAGAGAGAGGAAA 1230
 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
 1231 ATGTACCTGAAGACTGCTTCTCAGATGCCCTTACAAAGTCTTCCATTACCAAGTAAGATT 1290
 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
 1291 CATTTTCTGGGACTGAGAGTGAAACCCATACCAATCAGGCTTTTGAGATTTCTCTGTAT 1350
 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
 1351 GGCACCGTGGCCGAGAGTGAACATCCATTCATCTGCTGAGGTTCACCAATATGAG 1410
 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeu 380
 1411 ACCTACT 1470

QY 381 LysTrpLysSerAspSerTyPheSerTrpSerAspTrpTrpSerSerProGlyPheAla 400
 Db 1471 AAATGGAGAGTGTATCATCTTAGCTGGTGCAGACTGGTGGAGAGTCCCGGCTTCGCC 1530
 QY 401 IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
 Db 1531 ATTCAAGAGATCAGAGTAAAGCAGGAGAGACTCAGAAAAAGGTGATCTTCTGTTCTAGG 1590
 QY 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
 Db 1591 GAGAAAGTGCTCATTTGCAGAAAGGAAGGCACCTGCGGTATTGTGAAATGCCATGAC 1650
 QY 441 LysSerLeuAsnLysLysSerGly 448
 Db 1651 AAGTCTCTGAATAGAAAGTCAGGC 1674

RESULT 9

ADB47407

ID ADB47407 standard; cDNA; 4075 BP.

XX

AC ADB47407;

XX

DT 04-DEC-2003 (first entry)

XX

DE Human cDNA upregulated in dendritic cells SEQ ID NO 107.

XX

KW ss; gene; human; dendritic cells; high throughput; cancer;

XX

KW infectious disease; autoimmune disease; allergy;

XX

KW graft versus host disease; vaccine enhancing; gene therapy.

XX

OS Homo sapiens.

XX

FN US2003134283-A1.

XX

PD 17-JUL-2003.

XX

PF 03-OCT-2001; 2001US-00971392.

XX

PR 03-OCT-2000; 2000US-0237652P.

XX

PA (PETE/) PETERSON D P.

XX

PA (PEAR/) PEARSON C I.

XX

PA (COCK/) COCKS B G.

XX

PI Peterson DP, Pearson CI, Cocks BG;

XX

XX WPI; 2003-662509/62.

XX

XX Claim 1; SEQ ID NO 107; 28pp; English.

XX

CC The invention relates to a combination comprising cDNAs that are
 CC differentially expressed in dendritic cells (DC). Also included is a high
 CC throughput method for detecting differential expression of one or more
 CC cDNAs in a sample containing nucleic acids. The combination is useful for
 CC preparing a composition for diagnosing, treating and monitoring the
 CC treatment of cancer, infectious disease, autoimmunity, allergy or graft
 CC versus host disease, or for enhancing a vaccine. The present sequence
 CC represents a human cDNA upregulated in dendritic cells. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?docID=20030134283.

XX

SQ Sequence 4075 BP; 1168 A; 848 C; 938 G; 1121 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1-12e-235 Length: 4075
 Score: 2372.00 Matches: 448

Percent Similarity: 99.78% Conservative: 0
 Best Local Similarity: 99.78% Mismatches: 0
 Query Match: 99.45% Indels: 1
 DB: 10 Gaps: 0

US-10-019-341-3 (1-448) x ADB47407 (1-4075)

QY 1 AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
 Db 750 GCCGACCAAGAGAGATTTATCGACATCGAAGTAATTTGCCCTTAAGGACCCCTGAA 809
 QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
 Db 810 GACACAGCTGAGGACACTTGCACCTCATTCGCGAGTAGCAGAGTCCGTGGCTACCTGT 869
 QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTrpThrValThrGlyMet 60
 Db 870 CATTTTCATCACAGCAGCAAAACCTTCATGGTGATCCATGGCTGCGACGGTAACAGGAATG 929
 QY 61 TyrGluSerTrpValProLysLeuValAlaLeuTyrLysArgGluProAspSerAsn 80
 Db 930 TATGAGAGTTGGTGCCAAACTTTGTGGCGCCCTGTACAAGAGAACCCAGACTCCAAT 989
 QY 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
 Db 990 GTCAATTGTGGTGGACTGGCTGTACGGGCTCAGGAGCATTAACCCAGTGTCCGCGGCTAC 1049
 QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluPheAsn 120
 Db 1050 ACCAACTGGTGGGACAGATGTGGCCGGTTTATCACTGGATGGAGGAGGTTTAAAC 1109
 QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyValHisAlaIleGlyIle 140
 Db 1110 TACCCTCTGGACAATGTCCATCTCTTGGATACAGCTTGGAGCCATGCTCTGGCAAT 1169
 QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
 Db 1170 GCAGGAAGTCTGACCAATAAGAAAGTCAACAGATTACTGGCTCGATCCAGCTGGACCT 1229
 QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
 Db 1230 AACTTTGAGTATGCAGAAAGCCCGAGTCTCTTCTCTGATGATGCAGATTTTGTAGAC 1289
 QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
 Db 1290 GTCTTACACATTCACCAGAGGTCCTCGTGGTGAAGCATTTGGATTCAGAAACCACTT 1349
 QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
 Db 1350 GGGCATGTTGACATTTACCGAATGGAGGTACTTTTCAGCCAGGATGTAACTTTGGAGAA 1409
 QY 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
 Db 1410 GCTATCCGCGTGAITGCAGAGAGGACTTGGAGATGTGGACAGCTAGTGAAGTGCTCC 1469
 QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
 Db 1470 CACGAGCGCTCCATTCATCTCTTCATCGACTCTCTGTGAATGAAGAAATCCAAAGTAAG 1529
 QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysAtLys 280
 Db 1530 GCCTACAGGTGCGAGTTCCCAAGGAAGCCTTTGAGAAAGGCTCTGCTTGAGTTGTAAGAG 1589
 QY 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys 300
 Db 1590 AACCGCTGCAACAATCTGGGCTATGAGATCAATAAAGTCAGACCCCAAAAGACAGCAAA 1649
 QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
 Db 1650 ATGTACCTGAAGACCTGTTCTCAGATGCCCTACAAGTCTTCATTACCAAGTAAGATT 1709
 QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340

CC encoding a polypeptide which is believed to be cytostatic,
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein encoding sequence. The
CC present sequence is available on WIPOWEB and is not in the specification.
XX
SQ

Sequence 1584 BP; 450 A; 363 C; 388 G; 383 T; 0 U; 0 Other;

Alignment Scores: 3.52e-197 Length: 1584
Pred. No.: 1996.00 Matches: 387
Score: 82.17% Conservative: 0
Percent Similarity: 82.17% Mismatches: 84
Best Local Similarity: 83.69% Indels: 2
Query Match: 12 Gaps: 2

US-10-019-341-3 (1-448) x ADF28939 (1-1584)

Qy 1 AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
Db 82 GCCGACCAAGAGAGATTTATCGACATCGAAGTAATTTGCCCTAAGGACCCCTGAA 141
Qy 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
Db 142 GACACAGCTGAGGACATTCGCCACCTCATTCGCGAGTAGCAGAGTCCGCTACCTGT 201
Qy 41 HisPheAnHisSerSerLysThrPheMetValIleHisGlyThrValThrGlyMet 60
Db 202 CATTTCAATACACAGACGAAACCTTCATGGTGATCCCATGGCTGACGGTAACAGGAATG 261
Qy 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80
Db 262 TATGAGAGTTGGTGCCAAACTTTGTGGCGCCCTGTACAGAGAGAACCCAGACTCCAAAT 321
Qy 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
Db 322 GTCAATTTGTGGACTGGCTGTCACGGCTCAGGAGCATTTACCCAGTGTCCCGGGCTAC 381
Qy 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120
Db 382 ACCAAACTGGTGGACAGAGATGGCCCGGTTTATCACTGGATGAGGAGGAGTTTAACT 441
Qy 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyIle 140
Db 442 TACCCTCTGGACAAATGTCCATCTTTGGGATACAGCCTTGGAGCCCATGCTGTGGCAAT 501
Qy 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
Db 502 GCAGGAAGTCTGACCAATAAGAAAGTCAACAGAAATTAATGCTGATCCAGCTGGACCT 561
Qy 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
Db 562 AACTTTGAGTATGAGAGAGCCCGAGTGGTCTTCTCTGATGATGAGATTTTGTAGAC 621
Qy 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
Db 622 GTCTTTACACATTCACAGAGGGTCCCTGCTGGAAGCATTTGGAATCCAGAAACCAAGTT 681
Qy 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
Db 682 GGGCATGTGTACATTTACCCCAATGGAGTACTTTTCAGCCAGAGATGTAACATTTGGAGAA 741
Qy 221 AlaIleArgValIleAlaGluArgGlyLeuGly 231
Db 742 GCTATCCGCGATTTGCAGAGAGGAGGACTTGGAGACATGCCAAATGAACACTCTTTGTG 801
Qy 232 -----AspValAspGlnLeuVal 237
Db 802 AATTCTCCCGAGATACAATCTTGGTGTCTTTTACCCAGATGTGGACAGCTAGT 861
Qy 238 LysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluAsn 257

Db 862 AAGTGTCCACGAGCGCTCCATTCATCTCTTCATCGACTCTCTGTGTGATGAGAAAT 921
Qy 258 ProSerLysAlaTyrArgCysSerLysGluAlaPheGluLysGlyLeuCysLeuSer 277
Db 922 CCAAGTAAGCGCTACAGGTGCGATTTCAAGGAAGCCCTTTGAGAAGGGCTCTGCTTGA 981
Qy 278 CysArgLysAsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArg 297
Db 982 TGTAGAAGAAGCCGCTGCAACATCTGGGCTATGAGATCAATAAGTCAGAGCCAAAGA 1041
Qy 298 SerSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGln 317
Db 1042 AGCAGCAAAATGTACCTGAAGACTCGTTCTCAGATGCCCTACAAGTCTTCCATTACCA 1101
Qy 318 ValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIle 337
Db 1102 GTAAAGATTCATTTTCTGGACTGAGGTGAACCCCATCAATCAGGCCTTTGAGATT 1161
Qy 338 SerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSer 357
Db 1162 TCTCTGTATGGCACCGTGGCGAGGTGAGAACATCCCATTCACCTCTG----- 1209
Qy 358 ThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuMet 377
Db 1209 ----- 1209
Qy 378 LeuLysLeuLysTyrLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerPro 397
Db 1209 ----- 1209
Qy 398 GlyPheAlaIleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePhe 417
Db 1210 -----GTGATCTTC 1218
Qy 418 CysSerArgGluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLys 437
Db 1219 TGTCTTAGGAGAAAGTGTCTCATTTGCGAAGGAAGGACCTCGGTATTTGTGAAA 1278
Qy 438 CysHisAspLysSerLeuAsnLysLysSerGly 448
Db 1279 TGCCATGACAAAGTCTCTGATTAAGAAGTCAGGC 1311

RESULT 12

AAZ33576/C
ID AAZ33576 standard; cDNA; 2939 BP.

XX AC AAZ33576;

XX 08-DEC-1999 (first entry)

DE Human breast tumour-associated EST 36.

XX Expressed sequence tag; EST; human; breast; cancer; cytostatic;
XX medicaments; gene therapy; treatment; fat metabolism; ss.

XX Homo sapiens.

XX DEL9813835-AL.

XX 23-SEP-1999.

XX 20-MAR-1998; 98DE-01013835.

XX 20-MAR-1998; 98DE-01013835.

XX (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;

XX WPI; 1999-528979/45.

XX Human nucleic acid sequences and protein products from normal breast

PT tissue, useful for breast cancer therapy.

XX Claim 3; 124-125; 206pp; German.

CC This invention describes novel human nucleic acid sequences from normal
CC breast tissue which have cytostatic activity. The nucleic acid sequences
CC can be used to produce and isolate full-length gene sequences. They can
CC be used to express proteins, which can be used as tools to find an
CC activity against breast cancer. The sequences can be used in sense or
CC antisense form. They are especially useful for medicaments for gene
CC therapy to treat breast cancer and for treating illnesses associated with
CC fat metabolism. AA233541-233610 represent expressed sequence tags
CC described in the method of the invention

SQ Sequence 2939 BP; 857 A; 635 C; 545 G; 902 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1 43e-165 Length: 2939
Score: 1696.00 Matches: 323
Percent Similarity: 99.69% Conservative: 0
Best Local Similarity: 99.69% Mismatches: 0
Query Match: 71.11% Indels: 1
DB: 2 Gaps: 0

US-10-019-341-3 (1-448) x AA233576 (1-2939)

| | | | |
|----|------|--|------|
| QY | 126 | ValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaGlyLeuAlaGlySerLeuThr | 145 |
| DB | 2939 | GTCCATCTCTGGGATACAGCTTGGAGCCCATGCTGGCCATTCGAGAAAGTCTGACC | 2880 |
| QY | 146 | AsnLysLysVal-AsnArgLleThrGlyLeuAspProAlaGlyProAsnPhGluTyrAl | 165 |
| DB | 2879 | AATAGAAGTTCACACAAATTAAGTGGCTCGATCCAGCTGACCTAACTTGGATGCG | 2820 |
| QY | 165 | aGluAlaProSerArgLeuSerProAspAspAlaAspPheValAspValLeuHisThrPh | 185 |
| DB | 2819 | AGAAAGCCGAGTGGTCTTCTCCGATGTCAGATTTGTAGACGCTTACACACATT | 2760 |
| QY | 185 | eThrArgGlySerProGlyArgSerLleGlyLeuLysProValGlyHisValAspIl | 205 |
| DB | 2759 | CACAGAGGGTCCCTCGTGAAGCATTTGGATCCAGAACAGTTGGCCATGTGACAT | 2700 |
| QY | 205 | eTyrProAsnGlyThrPheGlnProGlyCysAsnLleGlyLeuAlaLleArgValIl | 225 |
| DB | 2699 | TTACCCGATGGAGGTACTTTTCAGCCAGGATGTAACATTCGAGAAGCTATCCGCGTAT | 2640 |
| QY | 225 | eAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSerHisGluArgSerIl | 245 |
| DB | 2639 | TGCAGAGAGAGGACTTGGAGATGTGGACCACTAGTGAAGTGTCCACAGCGCTCCAT | 2580 |
| QY | 245 | eHisLeuPheLeuAspSerLeuLeuAsnGluAsnProSerLysAlaTyrArgCysSe | 265 |
| DB | 2579 | TCATCTCTTCATCGACTCTCTGTGAATGAAGAAATCCAGTAAGCCCTACAGGTGCAG | 2520 |
| QY | 265 | rSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLysAsnArgCysAsnAs | 285 |
| DB | 2519 | TTCCAGGAGGCTTTGAGAAAGGCTCTCTGAGTTGTAGAAGAACCGCTGCACAA | 2460 |
| QY | 285 | nLeuGlyTyrGluLleAsnLysValArgAlaLysArgSerSerLysMetTyrLeuLysTh | 305 |
| DB | 2459 | TCTGGCTATGAGATCAATAAGTCAGAGCCAAAGAGCAGCAAAATGTACCTGAAGAC | 2400 |
| QY | 305 | rArgSerGlnMetProTyrLysValPheHisTyrGlnValLysLleHisPheSerGlyTh | 325 |
| DB | 2399 | TGTTCTCAGATGCCCTACAAAGTCTTCATACCAAGTAAGATTCATTTTCTGGGAC | 2340 |
| QY | 325 | rGluSerGluThrHisThrAsnGlnAlaPheGluLleSerLeuTyrGlyThrValAlaGl | 345 |
| DB | 2339 | TGAGAGTGAACCCCATACCAATCAGGCCCTTTCAGATTTCTGTATGGCAGCGTGC | 2280 |
| QY | 345 | uSerGluAsnLleProPheThrLeuProGluValSerThrAsnLysThrTyrSerPheLe | 365 |
| DB | 2279 | GAGTGAGACATCCCATTCCTCTGCTGAGGTTTCCACAAATAAGACCTACTCTCTCT | 2220 |

| | | | |
|----|------|---|------|
| QY | 365 | uileTyrThrGluValAspLleGlyGluLeuLeuMetLeuLysLeuLysTyrLysSerAs | 385 |
| DB | 2219 | AAATTTACACAGAGGTAGATATTGGAGAACTACTCATGTTGAAGCTCAATGGAGAGTGA | 2160 |
| QY | 385 | pSerTyrPheSerTyrSerAspTyrTrpSerSerProGlyPheAlaLleGlnLysLleAr | 405 |
| DB | 2159 | TTCATACTTTTAGCTGGTTCAGACTGGTGGAGCACTCCCGGCTTCGCCATTCAGAGATCAG | 2100 |
| QY | 405 | gVallLysAlaGlyGluThrGlnLysLysValLlePheCysSerArgGluLysValSerHi | 425 |
| DB | 2099 | AGTAAAGCAGGAGAGACTCAGAAAAAGGTGATCTTCTGTCTAGGAGAAAGTCTCTCA | 2040 |
| QY | 425 | sLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAspLysSerLeuAsnLy | 445 |
| DB | 2039 | TTTGCAAGAAAGGAGGACCTGGGTATTTGTGAATGCCATGACAGTCTCTGAATAA | 1980 |
| QY | 445 | sLysSerGly 448 | |
| DB | 1979 | GAAATCAGGC 1970 | |

RESULT 13

AA233605

ID AA233605 standard; cDNA; 2933 BP.

XX AC AA233605;

Alignment Scores:
Pred. No.: 5 73e-159 Length: 2933
Score: 1632.50 Matches: 319
Percent Similarity: 98.46% Conservative: 0
Best Local Similarity: 98.46% Mismatches: 4
Query Match: 68.45% Indels: 3

| | | | |
|-----------------|-----------------------------|--|-----|
| DB: | 2 | Gaps: | 0 |
| US-10-019-341-3 | (1-448) x AA233605 (1-2933) | | |
| QY | 126 | ValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThr | 145 |
| DB | 1 | GTCCATCTCTGGGATACAGCTTGGAGCCATCTGCTGGCATTTGAGGAAGTCTGACC | 60 |
| QY | 146 | AsnIysLysVal-AsnArgIleThrGlyLeuAspProAlaGlyProAsnPheGluIuYrAl | 165 |
| DB | 61 | AAATAGAAAGTTCAACAGATTACTGGCCCTCGATCCAGCTGGACCTTAACCTTTGAGTATGC | 120 |
| QY | 165 | gAluAlaProSerArgLeuSerProAspAspAlaAspPheValAspValLeuHisThrPh | 185 |
| DB | 121 | AGAAGCCCCAGTCTCTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGAT | 180 |
| QY | 185 | eThrArgGlySerProGlyArgSerIleGlyIleGlnLysProValGlyHisValAspIl | 205 |
| DB | 181 | CACAGAGGGTCCCTCGTGAAGCATTTGGAAATCCAGAAACCATTTGGGCATGTTGACAT | 240 |
| QY | 205 | eTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGluAlaIleArgValIl | 225 |
| DB | 241 | TTACCCGAATGGAGTACTTTTTCAGCCAGATGTAACATTCGAGAGAGCTATCCGCGTAT | 300 |
| QY | 225 | eAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSerHisGluArgSerIl | 245 |
| DB | 301 | TGCAGAGAGAGACTTGGAGATGTGACAGCTAGTGAAGTGTCTCCACGAGCGCTCCAT | 360 |
| QY | 245 | eHisLeuPheIleAspSerLeuLeuAsnGluLysProSerIysAlaTyrArgCysSe | 265 |
| DB | 361 | TCATCTCTTCATCGACTCTCTGTGAATGAAGAAATCAAGTAAGGCTACAGGTGCAG | 420 |
| QY | 265 | rSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLysAsnArgCysAsnAs | 285 |
| DB | 421 | TTCCAAGGAAGCCTTTGAGAAAGGGCTCTGCTTGTAGTTGTAGAAAGACCGCTGCAACA | 480 |
| QY | 285 | nLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLysMetTyrLeuLysTh | 305 |
| DB | 481 | TCGGGCTATGATGATCAATAAAGTCAGAGCCAAAGAGCAGCAAAATGATCTGAAGAC | 540 |
| QY | 305 | rArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIleHisPheSerGlyTh | 325 |
| DB | 541 | TCGTTCTCAGATGCCCTACAAAGTCTTCATATACCAAGTAAGATTCATTTTCTGGGAC | 600 |
| QY | 325 | rGluSerGlnThrHisThrAsnGlnAlaPheGluIleSerLeuTyrGlyThrValAlaGl | 345 |
| DB | 601 | TGAGAGTGAACCCATACCATCAGCCCTTGAGAT--TCTCTGTATGGCACCCTGGCGCA | 658 |
| QY | 345 | uSerGluAsnIleProPheThrLeuProGluValSerThrAsnLysThrTyrSerPheLe | 365 |
| DB | 659 | GAGTGAGAACATCCCATTCCTCTGCTGAAGTTTCCACAAATAGACCTTACTCTCTCT | 718 |
| QY | 365 | ulleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeuLysTrpLysSerAs | 385 |
| DB | 719 | AAATTTACACAGAGTAGATATTGGAGAACAC-CTCAAGTTGAGCTCAAATGGAGAGTGA | 777 |
| QY | 385 | pSerTyrPheSerTrpSerAspTrpTrpSerSerProGlyPheAlaIleGlnLysIleAr | 405 |
| DB | 778 | TTTATATTTAGTGTGTCAGACTGTGTGAGCAGTCCCGGCTTCGCCATTCAGAGATCAG | 837 |
| QY | 405 | gValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArgGlnLysValSerHi | 425 |
| DB | 838 | AGTAAAGCAGGAGAGACTCAGAAAAAAGGTGATCTTCTGTAGGGAGAAAGTGTCTCA | 897 |
| QY | 425 | sLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAspLysSerLeuAsnLy | 445 |
| DB | 898 | TTTTCAGAAAGAAAGGACCTGCGTATTGTGAAATGCCATGCAGAGTCTCTGGAATAA | 957 |
| QY | 445 | sLysSerGly | 448 |
| DB | 958 | GAGTTCAGGC | 967 |

| | |
|------------------------|--|
| ABL91801 | |
| ID | ABL91801 standard; DNA; 1503 BP. |
| XX | |
| AC | ABL91801; |
| XX | |
| DT | 11-JUL-2002 (first entry) |
| XX | |
| DE | Human lipase endothelial (LIPG) isogene coding sequence. |
| XX | |
| XX | Human; ds, gene; single nucleotide polymorphism; SNP; |
| KW | lipase endothelial isogene; LIPG; drug screening; atherosclerosis; |
| KW | cardiovascular disorder; LIPG haplotyping; LIPG genotyping. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| FH | Key |
| CDS | Location/Qualifiers |
| FT | 1. 1503 |
| FT | /tag= a |
| FT | /product= "Human lipase endothelial (LIPG) protein" |
| FT | /replace(12, A) |
| FT | allele |
| FT | /tag= b |
| FT | /standard_name= "Single nucleotide polymorphism" |
| FT | /replace(160, T) |
| FT | allele |
| FT | /tag= c |
| FT | /standard_name= "Single nucleotide polymorphism" |
| FT | /replace(332, T) |
| FT | allele |
| FT | /tag= d |
| FT | /standard_name= "Single nucleotide polymorphism" |
| FT | /replace(831, G) |
| FT | allele |
| FT | /tag= e |
| FT | /standard_name= "Single nucleotide polymorphism" |
| XX | |
| PN | WO200216397-A2. |
| XX | |
| PD | 28-FEB-2002. |
| XX | |
| PF | 17-AUG-2001; 2001WO-US026639. |
| XX | |
| PR | 25-AUG-2000; 2000US-0227825P. |
| XX | |
| PA | (GENA-) GENAISANCE PHARM INC. |
| XX | |
| PI | Duda A, Kazemi A, Klien SE, Messer C; |
| XX | |
| DR | WPI: 2002-292055/33. |
| DR | P-PSDB; AA014635. |
| XX | |
| PT | Novel genetic variants of Lipase, Endothelial isogenes, useful for |
| PT | improving efficiency and reliability in drug development for treating |
| PT | diseases associated with LIPG activity, e.g. atherosclerosis. |
| XX | |
| PS | Claim 25; Fig 2; 134pp; English. |
| XX | |
| CC | The invention comprises the DNA and amino acid sequence of the human |
| CC | lipase, endothelial (LIPG) isogene. Specifically, the invention relates |
| CC | to the discovery of 20 novel polymorphic sites within the LIPG gene. The |
| CC | LIPG coding sequence and protein are useful for screening drugs that can |
| CC | be used to treat atherosclerosis and other cardiovascular disorders. The |
| CC | LIPG coding sequence can also be used to haplotype and genotype the LIPG |
| CC | gene of an individual. The present DNA sequence represents the coding |
| CC | sequence of the human LIPG gene |
| XX | |
| SQ | Sequence 1503 BP; 381 A; 398 C; 396 G; 328 T; 0 U; 0 Other; |
| Alignment Scores: | |
| Pred. No.: | 2.34e-110 Length: 1503 |
| Score: | 1161.00 Matches: 216 |
| Percent Similarity: | 69.16% Conservative: 89 |
| Best Local Similarity: | 48.98% Mismatches: 118 |
| Query Match: | 48.68% Indels: 18 |
| DB: | 6 Gaps: 6 |
| US-10-019-341-3 | (1-448) x ABL91801 (1-1503) |

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 18:18:05 ; Search time 125 Seconds
(without alignments)

2547.467 Million cell updates/sec

Title: US-10-019-341-3

Perfect score: 2385

Sequence: 1 ADOORDFDIESKPAITPE.....GKAPAVFKCHDKSLNKSG 448

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Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Issued Patents NA -QWMT=fascap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0

-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human4.0.cdi

-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15

-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000

-USER=US10019341@cgn 1 1 69 @runat_22102004_120139_1636 -NCPU=6 -ICPU=3

-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:*

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4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*

5: /cgn2_6/ptodata/1/ina/6C.COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 1161 | 48.7 | 2565 | 3 | US-08-985-492-7 |
| 3 | 928 | 38.9 | 1035 | 3 | US-08-985-492-9 |
| 4 | 928 | 38.9 | 1065 | 3 | US-08-985-492-5 |
| 5 | 928 | 38.9 | 1382 | 3 | US-08-985-492-3 |
| 6 | 928 | 38.9 | 1510 | 4 | US-10-140-002-399 |
| 7 | 634 | 26.6 | 9734 | 3 | US-09-347-114A-80 |
| 8 | 461.5 | 19.4 | 1401 | 4 | US-09-411-132A-2 |
| 9 | 461.5 | 19.4 | 2352 | 4 | US-09-411-132A-1 |
| 10 | 451.5 | 18.9 | 1206 | 4 | US-09-513-999C-79 |
| 11 | 414 | 17.4 | 231 | 3 | US-08-905-124-4 |
| 12 | 363 | 15.2 | 1889 | 4 | US-09-799-451-90 |
| | | | | | Sequence 39, Appl |
| | | | | | Sequence 7, Appl |
| | | | | | Sequence 5, Appl |
| | | | | | Sequence 3, Appl |
| | | | | | Sequence 399, App |
| | | | | | Sequence 80, Appl |
| | | | | | Sequence 2, Appl |
| | | | | | Sequence 1, Appl |
| | | | | | Sequence 79, Appl |
| | | | | | Sequence 4, Appl |
| | | | | | Sequence 90, Appl |

ALIGNMENTS

RESULT 1

US-09-054-272-39

; Sequence 39, Application US/09054272

; Patent No. 6692909

; GENERAL INFORMATION:

; APPLICANT: Lander, Eric S.

; APPLICANT: Daley, George Q.

; APPLICANT: Cargill, Michele

; APPLICANT: Ireland, James S.

; APPLICANT: Rozen, Steven G.

; TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS

; TITLE OF INVENTION: IN VASCULAR PATHOLOGY GENES

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: MA

; COUNTRY: USA

; ZIP: 02173

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/054,272

; FILING DATE: 01-APR-1998

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Granahan, Patricia

; REGISTRATION NUMBER: 32,227

; REFERENCE/DOCKET NUMBER: WHI98-05

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| 13 | 328.5 | 13.8 | 1050 | 1 | US-08-180-209B-16 | Sequence 16, Appl |
| 14 | 328.5 | 13.8 | 1050 | 1 | US-08-385-745-16 | Sequence 16, Appl |
| 15 | 328.5 | 13.8 | 1050 | 3 | US-08-485-388-16 | Sequence 16, Appl |
| 16 | 328.5 | 13.8 | 1050 | 3 | US-08-474-853-16 | Sequence 16, Appl |
| 17 | 328.5 | 13.8 | 1050 | 3 | US-09-166-205B-16 | Sequence 16, Appl |
| 18 | 328.5 | 13.8 | 1050 | 5 | PCT-US94-02629-16 | Sequence 16, Appl |
| 19 | 327 | 13.7 | 3877 | 4 | US-09-054-272-54 | Sequence 81, Appl |
| 20 | 327 | 13.7 | 3877 | 4 | US-09-054-272-54 | Sequence 54, Appl |
| 21 | 320.5 | 13.4 | 856 | 4 | US-09-270-767-11560 | Sequence 11560, A |
| 22 | 306.5 | 12.9 | 1048 | 3 | US-09-166-205B-63 | Sequence 63, Appl |
| 23 | 306.5 | 12.9 | 1048 | 4 | US-09-806-658-1 | Sequence 1, Appl |
| 24 | 304 | 12.7 | 761 | 4 | US-09-270-767-14310 | Sequence 14310, A |
| 25 | 294 | 12.3 | 1341 | 1 | US-08-180-209B-26 | Sequence 26, Appl |
| 26 | 294 | 12.3 | 1341 | 1 | US-08-385-745-26 | Sequence 26, Appl |
| 27 | 294 | 12.3 | 1341 | 3 | US-08-485-388-26 | Sequence 26, Appl |
| 28 | 294 | 12.3 | 1341 | 3 | US-08-474-853-26 | Sequence 26, Appl |
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| 30 | 294 | 12.3 | 1341 | 5 | PCT-US94-02629-26 | Sequence 26, Appl |
| 31 | 282.5 | 11.8 | 1168 | 4 | US-09-270-767-662 | Sequence 662, App |
| 32 | 282.5 | 11.8 | 1168 | 4 | US-09-270-767-15944 | Sequence 15944, A |
| 33 | 276.5 | 11.6 | 579 | 4 | US-09-270-767-1889 | Sequence 1889, Ap |
| 34 | 276.5 | 11.6 | 579 | 4 | US-09-270-767-17171 | Sequence 17171, A |
| 35 | 259 | 10.9 | 430 | 4 | US-09-270-767-16345 | Sequence 16345, A |
| 36 | 259 | 10.9 | 430 | 4 | US-09-270-767-16345 | Sequence 11, Appl |
| 37 | 236 | 9.9 | 225 | 3 | US-08-985-492-11 | Sequence 11578, A |
| 38 | 236 | 9.9 | 225 | 3 | US-09-270-767-11578 | Sequence 27181, A |
| 39 | 192 | 8.1 | 558 | 4 | US-09-270-767-27181 | Sequence 90, Appl |
| 40 | 189 | 7.9 | 1889 | 4 | US-09-799-451-90 | Sequence 1, Appl |
| 41 | 173 | 7.3 | 367 | 3 | US-08-985-492-1 | Sequence 6, Appl |
| 42 | 169.5 | 7.1 | 8442 | 3 | US-09-272-032-6 | Sequence 27160, A |
| 43 | 146.5 | 6.1 | 570 | 4 | US-09-513-999C-80 | Sequence 80, Appl |
| 44 | 123 | 5.2 | 220 | 4 | US-09-270-767-27160 | Sequence 27160, A |
| 45 | 115.5 | 4.8 | 400 | 4 | US-09-513-999C-81 | Sequence 81, Appl |

Mon Oct 25 15:42:53 2004

TELECOMMUNICATION INFORMATION:

TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
TELEX:

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 3549 base pairs
TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 175...1599

OTHER INFORMATION:

US-09-054-272-39

Alignment Scores:

| Pred. No.: | 1.68e-277 | Length: | 3549 |
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| Score: | 2385.00 | Matches: | 448 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 4 | Gaps: | 0 |

US-10-019-341-3 (1-448) x US-09-054-272-39 (1-3549)

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|----|-----|--|-----|
| QY | 1 | AlaAspGlnArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu | 20 |
| DB | 256 | GCCGACCAAGAGAGATTTATCGACATCGAAGTAATTTGCCCTAAGGACCCCTGAA | 315 |
| QY | 21 | AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys | 40 |
| DB | 316 | GACACAGCTGAGGACACTTGCCACCTCATTCGCGAGTAGCAGAGTCCGTGCTACCTGT | 375 |
| QY | 41 | HisPheAsnHisSerSerLysThrPheMetValIleHisGlyThrValThrGlyMet | 60 |
| DB | 376 | CATTTCAATCATCAGCAGCAAAACCTTCATGGTGATCCATGGCTGGACGTTAACAGGATG | 435 |
| QY | 61 | TyrGluSerTyrValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn | 80 |
| DB | 436 | TATGAGAGTGGTGCCAAACCTTGTGGCGCCCTGTACAGAGAGAACACAGACTCCAAT | 495 |
| QY | 81 | ValIleValValAspThrLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr | 100 |
| DB | 496 | GTCAATTTGGTGACTGGCTGTACCGGCTCAGGAGCATTACCCAGTGTCCCGGGCTAC | 555 |
| QY | 101 | ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTyrMetGluGluGluPheAsn | 120 |
| DB | 556 | ACCAAACTGGTGGGACAGGATGTGGCCCGTTTATCAACTGGATGGAGGAGTTTAAAC | 615 |
| QY | 121 | TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyIle | 140 |
| DB | 616 | TACCTCTGTGACAAATGTCATCTCTTGGGATACAGCTTGGAGCCCATGCTGTGGCATT | 675 |
| QY | 141 | AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro | 160 |
| DB | 676 | GCAGGAAGTCTGACCAATAAGAAAGTCAACAGAAATTAATGCTCGATCCAGCTGGACCT | 735 |
| QY | 161 | AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp | 180 |
| DB | 736 | AACTTTGAGTATGCAAGAGCCCGAGTGTCTTCTCTCATGATGACGATTTGTAGAC | 795 |
| QY | 181 | ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal | 200 |
| DB | 796 | GTCTTACACATTCCACAGAGGGTCCCTGGTGGAGGATTTGAAATCCAGAAACCAAGTT | 855 |
| QY | 201 | GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu | 220 |
| DB | 856 | GGCATGTGACATTTACCGAATGGAGGTACTTTTCAGCCAGGATGTAACATTTGGAGAA | 915 |
| QY | 221 | AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer | 240 |

| | | | |
|----|------|---|------|
| DB | 916 | GCTATCCGGCTGATTGCAGAGACAGAGACTTGGAGATGTGGACCGACCTAGTGAAGTGTCC | 975 |
| QY | 241 | HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys | 260 |
| DB | 976 | CACGAGCGCTCCATTTATCTCTTCATCGACTCTCTGTTGAATGAAGAAATCCAAGTAAG | 1035 |
| QY | 261 | AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys | 280 |
| DB | 1036 | GCCTACAGGTGCAGTTCCTCAAGGAGCGCTTTGAGAAAGGCTCTCTTGAGTTGTAGAAAG | 1095 |
| QY | 281 | AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys | 300 |
| DB | 1096 | AACCGCTGCCAACATCTGGGCTATGAGATCAATAAAGTCAGAGCCAAAGAGCAGCAA | 1155 |
| QY | 301 | MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle | 320 |
| DB | 1156 | ATGTACCTGAAGACTCGTTCTCAGATGCCCTACAAAGTCTTCCATTACCAAGTAAAGATT | 1215 |
| QY | 321 | HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr | 340 |
| DB | 1216 | CATTTTCTGGGACTGAGAGTGAAACCATACCAATCAGGCTTTGAGATTCTCTGTAT | 1275 |
| QY | 341 | GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys | 360 |
| DB | 1276 | GGCACCGTGGCGGAGAGTGAACATCCCATTCATCTGCTGCTGAAGTTTCCACAATAAG | 1335 |
| QY | 361 | ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeu | 380 |
| DB | 1336 | ACCTACTCTCTTCTTAATTTACACAGAGGTAGATATTGAGAACTACTCATGTGAAGCTC | 1395 |
| QY | 381 | LysTrpLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerSerProGlyPheAla | 400 |
| DB | 1396 | AAATGGAAGAGTGATTCATCTTACTAGCTGGTCAGACTGGTGAGCAGTCCCGCTTCGCC | 1455 |
| QY | 401 | IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg | 420 |
| DB | 1456 | ATTCAGAAGATCAGAGTAAAGCAGAGAGACTCAGAAAAGGTGATCTCTGTTCTAGG | 1515 |
| QY | 421 | GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp | 440 |
| DB | 1516 | GAGAAAGTGTCTCATTTTGCAGAAAGGAAAGGACCTCGCGTATTTGTGAATGCCATGAC | 1575 |
| QY | 441 | LysSerLeuAsnLysLysSerGly | 448 |
| DB | 1576 | AAGTCTCTGAATAAGAGTCAGGC | 1599 |

RESULT 2

US-08-985-492-7

Sequence 7, Application US/08985492

Patent No. 6395530

GENERAL INFORMATION:

APPLICANT: Jaye, Michael C.

APPLICANT: Doan, Kim-Anh T.

APPLICANT: Krawiec, John A.

APPLICANT: Lynch, Kevin J.

APPLICANT: Amin, Dilip V.

APPLICANT: South, Victoria J.

TITLE OF INVENTION: LLG POLYPEPTIDES OF THE TRIACYLGLYCEROL

TITLE OF INVENTION: LIPASE FAMILY, AND COMPOSITIONS AND METHODS FOR THEIR USE

NUMBER OF INVENTION: IN ENZYMIC HYDROLYSIS, AND PROTEIN AND GENE THERAPIES

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESS: Rhone-Poulenc Rorer Inc.

STREET: 500 Arcola Rd. 3043

CITY: Collegeville

STATE: PA

COUNTRY: USA

ZIP: 19426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/985,492
/ FILING DATE:
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fehliner Ph.D., Paul F.
/ REGISTRATION NUMBER: 35,135
/ REFERENCE/POCKET NUMBER: A2582-US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (610)454-3839
/ TELEFAX: (610)454-3808
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2565 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 252..1754
/ US-08-985-492-7

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Alignment Scores:

| | | | |
|------------------------|----------|---------------|------|
| Pred. No.: | 1.2e-129 | Length: | 2565 |
| Score: | 1161.00 | Matches: | 216 |
| Percent Similarity: | 69.16% | Conservative: | 89 |
| Best Local Similarity: | 48.98% | Mismatches: | 118 |
| Query Match: | 48.68% | Indels: | 18 |
| DB: | 3 | Gaps: | 6 |

US-10-019-341-3 (1-448) x US-08-985-492-7 (1-2565)

| | | | |
|----|-----|--|-----|
| Qy | 13 | LysPheAlaLeuArgThrProGluAspThrAlaGluAspThrCysHisLeuLeuProGly | 32 |
| Db | 399 | AGGTTTAACTCCGACCTCCGAAGACCAGGACATGAAGATGCTACTCTCCCGTCGC | 458 |
| Qy | 33 | VallAlaGluSerValAlaThrCysHisPheAsnHisSerSerLysThrPheMetValIle | 52 |
| Db | 459 | CACAGCCAGCCCTTAGAAGACTGCAGTTTCAACATGCAGCTAAAACCTTTTCATCAT | 518 |
| Qy | 53 | HisGlyTrpThrValThrGlyMetTyrGluSerTrpValProLysLeuValAlaAlaLeu | 72 |
| Db | 519 | CACGGATGGACGATGACGGGTATCTTTGAAAACCTGGCTGCACAACTCGTGTCAGCCCTG | 578 |
| Qy | 73 | TyrLysArgGluProAspSerAsnValIleValAspTrpLeuSerArgAlaGlnGlu | 92 |
| Db | 579 | CACACAGAGAGAAAGCGCCAATGTAGTTGTGGTTGACTGGCTCCCTCGCCACCACG | 638 |
| Qy | 93 | HisTyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAlaArgPheIle | 112 |
| Db | 639 | CTTTACACGGATGGCGTCAATAATACAGGGTGGGACACAGCATTTGCCAGGATGTC | 698 |
| Qy | 113 | AsnTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSer | 132 |
| Db | 699 | GACTGGCTGCAGGAGAAAGCAGATTTCCTCCGGATGTCCACTTGATCGGTACAGC | 758 |
| Qy | 133 | LeuGlyAlaHisAlaAlaGlyTleAlaGlySerLeuThrAsnLysValAsnArgIle | 152 |
| Db | 759 | CTCGAGCGCACGTGGCCGGGTATGCAGGCAACTTCGTGAAGAGAACGGTGGCGGATC | 818 |
| Qy | 153 | ThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSer | 172 |
| Db | 819 | ACAGGTTTGATCTCTCCCGGCCCATGTTTGAGGGGCGACATCCACAGAGGCTCTCT | 878 |
| Qy | 173 | ProAspAlaAspPheValAspValLeuHisThrPheThrArgGlySerProGlyArg | 192 |
| Db | 879 | CCGAGCATGCAGATTTGTGGATGTCTCCACACTACACGGCT--TCCTCGGCTTG | 935 |
| Qy | 193 | SerIleGlyLeuGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPhe | 212 |
| Db | 936 | AGCATTTGGTATTACAGTCCCTGTGGGCCCATTCATGACATCTACCCCAATGGGGTGACTTC | 995 |

RESULT 3

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US-08-985-492-9
/ Sequence 9, Application US/08985492
/ Patent No. 6395530
/ GENERAL INFORMATION:
/
/ APPLICANT: Jaye, Michael C.
/ APPLICANT: Doan, Kim-Anh T.
/ APPLICANT: Krawiec, John A.
/ APPLICANT: Lynch, Kevin J.
/ APPLICANT: Amin, Dilip V.
/ APPLICANT: South, Victoria J.
/
/ TITLE OF INVENTION: LG POLYPEPT
/ TITLE OF INVENTION: LIPASE FAMILY
/ TITLE OF INVENTION: IN ENZYMATI
/
/ NUMBER OF SEQUENCES: 31
/
/ CORRESPONDENCE ADDRESS:
/
/ ADDRESSEE: Rhone-Poulenc Rorene
/ STREET: 500 Arcola Rd. 3C43
/ CITY: Collegeville
/ STATE: PA
/ COUNTRY: USA

```

[illegible]

```

628 CCGGACGATGCAGATTCTTTGGTGTCTCCTCCACACCCTACACGCGT---TCCTTCGGCTTG 584
193 SerIleGlyLeuGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPhe 212
685 AGCATTTGGTATTTCAGATGCCCTGTGGCCACAAATTGACATCTACCCCCAATGGGGTGACTTC 744
213 GlnProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAsp 232
745 CAGCCAGCGCTGTGACTCAACGATGCTCTGGGATCAATTGCA-----TATGGAACA 795
233 ValAspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeu 252
796 ATCACAGAGGTGTATAAATGTGAGCATGAGCGAGCGCTCCACCTCTTTGTTGACTCTCTG 855
253 LeuAsnGluGluAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLys 272
856 GTGAATCAGGACAACCGAGTTTTCCCTTCCAGTGCACTGACTCCCATCGCTTCAAAGAAG 915
273 GlyLeuCysLeuSerCysArgLysAsnArgCysAsnAsnLeuGlyTyrGluIleAsnLys 292
916 GGATCTCTGTCTGAGCTGCCGCAAGAACCGTCTTAATAGCATTTGGCTACAAATGCCAAGAAA 975
293 ValArgAlaLysArgSerSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLys 312
976 ATGAGGAACAAGAGGAAACAGCAAAATGTACTTAAAAACCCGGCGCGCATG CCTTTTCAGA 1035

RESULT 4
US-08-985-492-5
; Sequence 5, Application US/08985492
; Patent No. 6395530
; GENERAL INFORMATION:
; APPLICANT: Jaye, Michael C.
; APPLICANT: Doan, Kim-Anh T.
; APPLICANT: Krawiec, John A.
; APPLICANT: Lynch, Kevin J.
; APPLICANT: Amin, Dilip V.
; APPLICANT: South, Victoria J.
TITLE OF INVENTION: LLG POLYPEPTIDES OF THE TRIACYLGlycerOL
TITLE OF INVENTION: LIPASE FAMILY, AND COMPOSITIONS AND METHODS FOR THEIR
TITLE OF INVENTION: IN ENZYMATIC HYDROLYSIS, AND PROTEIN AND GENE THERAPIES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Rd. 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,492
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Fehner Ph.D., Paul F.
REGISTRATION NUMBER: 35,135
REFERENCE/DOCKET NUMBER: A2582-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3839
TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1065 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: CDS

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; LOCATION: 1..1065
US-08-985-492-5
Alignment Scores:
Pred. No.: 4,12e-102 Length: 1065
Score: 928.00 Matches: 165
Percent Similarity: 75.33% Conservative: 61
Best Local Similarity: 55.00% Mismatches: 70
Query Match: 38.91% Indels: 4
DB: 3 Gaps: 2

US-10-019-341-3 (1-448) x US-08-985-492-5 (1-1065)
QY 13 LysPheAlaLeuArgThrProGluAspThrAlaGluAspThrCysHisLeuIleProGly 32
Db 148 AGGTTTAACCTCGCACCTCCAGGACCCAGAGCATGAAGATGCTTCTCCGTCGCGC 207
QY 33 ValAlaGluSerValAlaThrCysHisPheAsnHisSerSerLysThrPheMetValIle 52
Db 208 CACAGCCAGCCCTTGAAGACTGCAGTTTCAACATGCAGACTAAACCTTTTCATCAT 267
QY 53 HisGlyTyrThrValThrGlyMetTyrGluSerTyrValProLysLeuValAlaLeu 72
Db 268 CACGATGACGATGAGCGGTATCTTTGAAACTGGCTGCACAAACTCGTGTACGCGCTG 327
QY 73 TyrLysArgGluProAspSerAsnValIleValValAspTyrLeuSerArgAlaGlnGlu 92
Db 328 CACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 387
QY 93 HisTyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAlaArgPheIle 112
Db 388 CTTTACAGGATGGGTGATTAATACAGGAGTGTGGGACACAGCATTTGCCAGATGCTC 447
QY 113 AsnTyrMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSer 132
Db 448 GACTGGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 507
QY 133 LeuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysLysValAsnArgIle 152
Db 508 CTCGAGCGCAGTGGCGGCTATGCAGGCACTTCGTAAGAGAACGGTGGCGGCAATC 567
QY 153 ThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSer 172
Db 568 ACAGTTTGGATCTCGCGGCGCCATGTTTGAAGGGCGGACATCCACAGAGAGCTCTCT 627
QY 173 ProAspAlaAspPheValAspValLeuHisThrArgGlySerProGlyArg 192
Db 628 CCGGACGATGCAGATTTTGGATGTCCTCCACACCTACACGGCT---TCCTTCGGCTTG 684
QY 193 SerIleGlyLeuGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPhe 212
Db 685 AGCATTTGGTATTCAGATGCTGTGGGCGCCACATTCACATCTACCCCAATGGGGTGACTTC 744
QY 213 GlnProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAsp 232
Db 745 CAGCCAGGCTGTGAGCTCAACGATGCTTGGGATCAATTCGA-----TATGGAACA 795
QY 233 ValAspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeu 252
Db 796 ATCAGAGAGGTGTAAATGTGAGATGAGCGAGCGCTCCACCTCTTTGTGACTCTCTG 855
QY 253 LeuAsnGluGluAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLys 272
Db 856 GTGAATCAGAGCAAGCGAGTTTGGCTTCCAGTGCAGCTACCTCCCAATCGCTTCAAAAG 915
QY 273 GlyLeuCysLeuSerCysArgLysAsnArgCysAsnAsnLeuGlyTyrGluIleAsnLys 292
Db 916 GGAATCTGCTGAGCTGCGCGAAGAACCGTGTGTAATAGCATTTGGCTTACATGCCAAGAAA 975
QY 293 ValArgAlaLysArgSerSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLys 312
Db 976 ATGAGGAACAGAGGAGAACGAAAAATGTATACCTAAAAAACCCGGCGAGCATGCTTTTCA 1035
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RESULT 5
US-08-985-492-3
; Sequence 3, Application US/08985492
; Patent No. 6395530
; GENERAL INFORMATION:
; APPLICANT: Jaye, Michael C.
; APPLICANT: Doan, Kim-Anh T.
; APPLICANT: Krawiec, John A.
; APPLICANT: Lynch, Kevin J.
; APPLICANT: Amin, Dilip V.
; APPLICANT: South, Victoria J.
; TITLE OF INVENTION: LLG POLYPEPTIDES OF THE TRIACYLGLYCEROL
; TITLE OF INVENTION: LIPASE FAMILY, AND COMPOSITIONS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd. 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,492
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Fehlnher Ph.D., Paul F.
; REGISTRATION NUMBER: 35,135
; REFERENCE/DOCKET NUMBER: A2582-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3839
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1382 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 312..1370
; US-08-985-492-3
Alignment Scores:
Pred. No.: 6,45e-102 Length: 1382
Score: 928.00 Matches: 165
Percent Similarity: 75.33% Conservative: 61
Best Local Similarity: 55.00% Mismatches: 70
Query Match: 38.91% Indels: 4
DB: 3 Gaps: 2
US-10-019-341-3 (1-448) x US-08-985-492-3 (1-1382)
QY 13 LysPheAlaLeuArgThrProGluAspThrAlaGluAspThrCysHisLeuIleProGly 32
Db 459 AGGTTTAACCTCGCACCTCCAGGACCCAGAGCATGAAGATGCTTCTCCGTCGCGC 518
QY 33 ValAlaGluSerValAlaThrCysHisPheAsnHisSerSerLysThrPheMetValIle 52
Db 519 CACAGCCAGCCCTTGAAGACTGCAGTTTCAACATGCAGACTAAACCTTTTCATCAT 578
QY 53 HisGlyTyrThrValThrGlyMetTyrGluSerTyrValProLysLeuValAlaLeu 72
Db 579 CACGATGACGATGAGCGGTATCTTTGAAACTGGCTGCACAAACTCGTGTACGCGCTG 638
QY 73 TyrLysArgGluProAspSerAsnValIleValValAspTyrLeuSerArgAlaGlnGlu 92

;; CURRENT FILING DATE: 2002-05-06
;; Prior Application removed - See Palm or File Wrapper
;; NUMBER OF SEQ ID NOS: 550
;; SEQ ID NO 399
;; LENGTH: 1510
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-10-140-002-399

Alignment Scores: 7.51e-102 Length: 1510
Pred. No.: 928.00 Matches: 165
Score: 928.00 Conservative: 61
Percent Similarity: 75.33% Mismatches: 70
Best Local Similarity: 55.00% Indels: 4
Query Match: 38.91% Gaps: 2
DB:

US-10-019-341-3 (1-448) x US-10-140-002-399 (1-1510)

QY 13 LysPheAlaLeuArgThrProGluAspThrAlaGluAspThrCysHisLeuLeuProGly 32
Db 370 AGTTTAACTCCGACCTCCAGGACCCAGAGCATGAAGATGCTACTCTCCGTCGCG 429
QY 33 ValAlaGluSerValAlaThrCysHisPheAsnHisSerSerLysThrPheMetValIle 52
Db 430 CACAGCCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAACCTTTTTCATCAT 489
QY 53 HisGlyTrpThrValThrGlyMetTrpValProLysLeuValAlaLeu 72
Db 490 CACGATGCGATGCGGCTATCTTGAAACTGGCTGCACAACTCGTGACGCTG 549
QY 73 TyrLysArgGluProAspSerAsnValIleValValAspTrpLeuSerArgAlaGlu 92
Db 550 CACACAAGAGAGAAAGACGCCAATGTAGTTGGTTGACTGGCTCCCTCCGCTG 609
QY 93 HisTrpProValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAlaArgPheIle 112
Db 610 CTTTACAGGATCGCGTCAATAATACAGGGTGGTGGGACACAGCATTCAGGATGCTC 669
QY 113 AsnTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSer 132
Db 670 GACTGCTGCAGAGAGAGACGATTTTCTCTCGGGAATGTCCACTTGTATCGGTACAGC 729
QY 133 LeuGlyValAlaAlaGlyIleAlaGlySerLeuThrAsnLysLysValAsnArgIle 152
Db 730 CTCGAGCGACGTCGCGGCTATGATGAGCAACTTCGTGAAAGAGACGGTGGCCGAATC 789
QY 153 ThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSer 172
Db 790 ACAGGTTTGGATCCTCGCGGCGCCATGTTTGAAGGGGCGCACATCCACAGAGGCTCTCT 849
QY 173 ProAspAlaAspPheValAspValLeuHisThrPheThrArgGlySerProGlyArg 192
Db 850 CCGGAGATGCGATTTTGGGATGCTCTCCACACCTACACGCGT---TCCTCGGCTTG 906
QY 193 SerIleGlyIleGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPhe 212
Db 907 AGCATTTGGTATTTCAGATGCTGTGGGCCACATGACATCTACCCCAATGGGGGTGACTTC 966
QY 213 GlnProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAsp 232
Db 967 CAGCCAGGCTGTGGACTCAACGATGCTTGGGATCAATTGCA-----TATGGAACA 1017
QY 233 ValAspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerIleu 252
Db 1018 ATCAGAGGTGGTAAATGTGACATGAGGAGCGCTCCACCTCTTTTGTGACTCTCTG 1077
QY 253 LeuAsnGluGluAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLys 272
Db 1078 GTGAATCAGGCAAGCGGAGTTTGGCTTCCAGTGCATGACTCCACTCAATCGCTTCAAAAG 1137
QY 273 GlyLeuCysLeuSerCysArgLysAsnArgCysAsnLeuGlyTyrGluIleAsnLys 292

Db 639 CACACAGAGAGAAAGCGCAATGATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 698
QY 93 HisTrpProValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAlaArgPheIle 112
Db 699 CTTTACAGGATCGCGTCAATAATACAGGCTGGTGGACACAGCATTCACGATGCTC 758
QY 113 AsnTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSer 132
Db 759 GACTGGCTGAGAGAGAGAGAGATTTTCTCTCGGATGTCCACTTGATCGGCTACAGC 818
QY 133 LeuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysLysValAsnArgIle 152
Db 819 CTCGAGCGCACGTCGCGGCTATGAGGCAACTTCGTGAAAGAGAAACGGTGGCGCAATC 878
QY 153 ThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSer 172
Db 879 ACAGTTTGGATCCTCGCGGCGCCATGTTTGAAGGGGCGCACATCCACAGAGGCTCTCT 938
QY 173 ProAspAlaAspPheValAspValLeuHisThrPheThrArgGlySerProGlyArg 192
Db 939 CCGGAGATGCGATTTTGGATGCTCTCCACACCTACACGCGT---TCCTTCGCGCTG 995
QY 193 SerIleGlyIleGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPhe 212
Db 996 AGCATTTGATTCAGATGCTGTGGCCACATTCATCTACCCCAATGGGGGTGACTTC 1055
QY 213 GlnProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAsp 232
Db 1056 CAGCCAGGCTGTGGACTCAACGATGCTTGGGATCAATTGCA-----TATGGAACA 1106
QY 233 ValAspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerIleu 252
Db 1107 ATCAGAGGTGGTAAATGTGAGCATGAGCGGCGCTCCACTCTTTTGTGACTCTCTG 1166
QY 253 LeuAsnGluGluAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLys 272
Db 1167 GTGAATCAGGCAAGCGGAGTTTTCCTTCCAGTGACGACTCCCAATCGCTTCAAAAG 1226
QY 273 GlyLeuCysLeuSerCysArgLysAsnArgCysAsnLeuGlyTyrGluIleAsnLys 292
Db 1227 GGGATCTGCTGAGTGGCGCGCAAGACCGTTTGTATAGCATTGGCTACATGCCAAGAAA 1286
QY 293 ValArgAlaLysArgSerSerLysMetTyrLeuIleThrArgSerGlnMetProTyrLys 312
Db 1287 ATGAGGAAACAGAGGAGACGAAATGTACTAAACCGGCGGCGGATGCTTTCAGA 1346

RESULT 6
US-10-140-002-399
; Sequence 399, Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Zhou, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C59
; CURRENT APPLICATION NUMBER: US/10/140,002

Db 1138 GGGATCTGCTGAGCTGCCGACGACCGTTGTAATAGCATTTGGCTACAATGCCAGAAA 1197
QY 293 ValArgAlaLysArgSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLys 312
Db 1198 ATGAGGACAGAGGACAGCAAAATGCTCTAAACCCCGGCGAGCATGCGCTTTCAGA 1257

RESULT 7

US-09-347-114A-80
; Sequence 80, Application US/09347114A
; Patent No. 6297014
; GENERAL INFORMATION:
; APPLICANT: Kent D. Taylor (Inventor)
; APPLICANT: Karen T. Scheuner (Inventor)
; APPLICANT: Jerome I. Rotter (Inventor)
; APPLICANT: Huiying Yang (Inventor)
; TITLE OF INVENTION: Genetic Test to Determine
; FILE OF INVENTION: No. 6297014-responsiveness to Statin Drug Treatment
; FILE REFERENCE: P07 41878
; CURRENT APPLICATION NUMBER: US/09/347,114A
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 9734
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-347-114A-80

Alignment Scores:
Pred. No.: 6,92e-65 Length: 9734
Score: 634.00 Matches: 196
Percent Similarity: 21.27% Conservative: 2
Best Local Similarity: 21.05% Mismatches: 4
Query Match: 26.58% Indels: 730
DB: 3 Gaps: 2

US-10-019-341-3 (1-448) x US-09-347-114A-80 (1-9734)

QY 111 PheIleAsnTrpMetGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGly 130
Db 122 TTTCTTTTCTCCAAAGAGAGAGGTTTAACTACCTCTGGCAATGTCTCTTGGA 181
QY 131 TyrSerLeuGlyAlaHisAlaAlaGlyLeuAlaGlySerLeuThrAsnLysValAsn 150
Db 182 TACAGCCTTGAGGCCATGCTGCTGGCATTGCGAGAGTCTGACCAATAGAAAGTCAAC 241
QY 151 ArgIleThrGlyLeu----- 155
Db 242 AGAATTACTGGTAA-GAAAGCAATTCGTTGGTCTTATCATAGAGGTGAAAGACTGTC 300
QY 155 ----- 155
Db 301 ATTCTGAGAGAGATCAGAACAAATTTGTTAAATACCCCATGTCATGTGGTCTCTCCCG 360
QY 155 ----- 155
Db 361 GAGACATGACCAGCCTTGATATCTCATTTAGGGCTCTTTATTAGGGATAAGAAAAA 420
QY 155 ----- 155
Db 421 CACAGAGGCTCTCACTGGCTTACTATCTCACTGGCAATGACAGAAATAAAGCATTA 480
QY 155 ----- 155
Db 481 CACAAATGCTGCAGATTCTCTGGAGCCCTGTTTCTCCCACTCTCAGCTCTGTGT 540
QY 155 ----- 155
Db 541 TTAGTAGTGTAAATGCATCATCAGTACTAGGAGAAAGAGAGCAATTCAGAGGCC 600
QY 155 ----- 155
Db 601 ACTTCGAAAGAGACCGCTCATCTAGGAAAGGTGTGGCATATACACAGAGAGAAAGAAC 660

QY 155 ----- 155
Db 661 CACCACCTGTTTATACATCTTCTCGACATATTTCAGAAATATCTACAAAAGAAATCCAGC 720
QY 155 ----- 155
Db 721 CATCTGAGTGGAAATGCTGCATAAGGCTAGTTTAAAGAGACTCAAAATTCATTTTAGAAG 780
QY 155 ----- 155
Db 781 GAGCCAAGCCTCTTTTATGTCTCTCTAAAGTAAAGATACCATGACTGTAGATAGGAGCT 840
QY 155 ----- 155
Db 841 AATAAGAAATCTAAATAGTGCAGAGTGCATTCAAATGATGAGCAGTGCATGCGAATGTCA 900
QY 156 ----- AspPro 157
Db 901 TACGAATGGAAATTTACAAATCTGTCTCTCTCTTTTCCCTTTTAAAGGCCTCGATCCA 960
QY 158 AlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAlaAsp 177
Db 961 GCTGGACCTTAACTTTGAGTATGCAAGCCCGAGTCTCTCTCTCTGATGATGAGAT 1020
QY 178 PheValAspValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGln 197
Db 1021 TTTGTAGAGCTTTTACACACATTCACAGAGGCTCCCTGGTGGAGCAATTCGAATCCAG 1080
QY 198 LysProValGlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsn 217
Db 1081 AAACCAAGTGGCAGTGTGACATTTACCCGAATGAGGACTTTTTCGCCAGGATGTAAC 1140
QY 218 IleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGly----- 231
Db 1141 ATTGGAGAGCTATCCGCGTGAATTCGACAGAGAGGACTTTGGAGGTAAATATTATTAGAA 1200
QY 231 ----- 231
Db 1201 GCGAATTAATGTGACTCTTATCTTAACCTTATGACCAATGTCTCTACTAGTAGCT 1260
QY 231 ----- 231
Db 1261 TCAAAGTATGTAGTTTTCATATACACATTTGGCCAAATTAATGTTCTGAAGAAATCTGCA 1320
QY 231 ----- 231
Db 1321 ATGTTCAAGATGACCACTTTAGAGCCAGGACAGACCATTTTATCTTTTATTACTATA 1380
QY 231 ----- 231
Db 1381 CTGTAGGCTACATGAGCAGTGCATTTACAGTAGCAGAAAGAAAGGGTGGATTTTAGAC 1440
QY 231 ----- 231
Db 1441 AGGAAGACTCCACTGACCTCAATAATGGCATCATATAATGCTATCTGGCCACATGTTGTC 1500
QY 231 ----- 231
Db 1501 ATACCTTGAATGTAGTGCAGAACCCAAATGGAAGAATTTTAGATGTTTACTGGAACAGAAGA 1560
QY 231 ----- 231
Db 1561 TGTTAATTAGCATAAATCTTCCAAATGTTTCAAGACATAATGTAGCTTAATGTTTACT 1620
QY 231 ----- 231
Db 1621 TTAATAATGTTAGCTGTGTGTTAAATTTATGATTTTGTGTTTGTGTTTGTGATAGAG 1680
QY 231 ----- 231
Db 1681 TCTTATTCTATTGCCCAAGCTGGGTGTCAGTACACAATTCACAGGAGCTTGCAATGTC 1740

QY 231 ----- 231
Db 1741 CCAGGCTGCTCAAACTCCTGGCCCTCAAGTGATCTCTCTGCTCAGCCTCCCAAGATTC 1800
QY 231 ----- 231
Db 1801 TGGGATTGACGCTGTGAGCCACCACGCCCGCTTACGATTATTTTAAAGGCCCTTGC 1860
QY 231 ----- 231
Db 1861 ATACTTTATAGACATTGGGACCTACCTAGGATATCTCTGTTATTTTGTGACGTAATAG 1920
QY 231 ----- 231
Db 1921 AACTTAGAGCATATTTACTATTTTCGATTGTCTTAAACTTTACAGGAATCAATCT 1980
QY 231 ----- 231
Db 1981 TATGCCATTGCTGATTATTTCTATGTTTATTAAGAGAGTGTAGTAGGGCAGA 2040
QY 231 ----- 231
Db 2041 ACCCTCAATTGACATATATCAATGATAAATAACAATTCATTTAAACAATTACCTCTTA 2100
QY 231 ----- 231
Db 2101 AGATGTGTTTCTAGAAATACAAATGTCTTAACTTACAGTTTCCAACTTTACAATTG 2160
QY 231 ----- 231
Db 2161 GGCTGTACACATTTTAAGTTGAGAAGCAGTGATGTTTGACCTTAAACTTTTGACA 2220
QY 231 ----- 231
Db 2221 TTATGATGGTTTGGGGTATTAAAGTGATTTTGACTTTACAGTATTTTGACTTATGAA 2280
QY 231 ----- 231
Db 2281 GAATTTATTGTAAGCAAGGGCAGGTATATGTTTCTAGAGCACCTAGAGTGTAGAC 2340
QY 231 ----- 231
Db 2341 ACTTTCAATGTAAGAGAGATGAGATAAACAAGGAATACACCTCCACCTTGGAGGCT 2400
QY 231 ----- 231
Db 2401 TATTACAGCTTCATAACATCTATATAATAAAGAACACAAAAGTCAAAATTCCTCG 2460
QY 231 ----- 231
Db 2461 TGAACCTTGCAACTTTCACCTCTCTTGAAGTGGGTGGGCGCGCTACCACCAAGATATCTCC 2520
QY 231 ----- 231
Db 2521 TGAATAGGCGCTACAAATCATAAATGACAGGACTATATCTCTGGGTGATTTACTCTAA 2580
QY 231 ----- 231
Db 2581 CACCACATCTCACCATTATTTAGACATGCCAAATGAAACACTTTTGTGAATTTCTGCCGA 2640
QY 232 ----- AspValAspGlnLeuValLysCysSerHis 241
Db 2641 GATACAACTCTGGTGTCTCTTTTATCCAGATGTGGCAGCTAGTGAAGTGTCTCCAC 2700
QY 242 GluArgSerIleHisLeuPheIleAspSerLeuAsnGluGluAsnProSerIleAala 261
Db 2701 GAGCGCTCCATTCATCTCTCACTGCTCTCTGTTGAATGAAGAAATCCAAAGTAAAGGCC 2760
QY 262 TyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLysAsn 281
Db 2761 TACAGGTGCACTTCCAGGAAGCCTTTGAGAAAGGCTCTGCTTGGTGTGAGTGAAGAAC 2820
QY 282 ArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLysMet 301

Db 2821 CGCTGCAACAATCTGGGCTATGAGATCAATAAAGTTCAGCCAAAGACGACGAATG 2880
QY 302 TyrIleuLysThrArgSerGlnMetProTyrLys 312
Db 2881 TACCTGAAGACTCGTCTCAGATGCCCTACAAA 2913
RESULT 8
US-09-411-132A-2
; Sequence 2, Application US/09411132A
; Patent No. 6558936
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: No. 6558936el Human Lipase Proteins, Nucleic Acids Encoding
; TITLE OF INVENTION: Then, and Uses of Both of These
; FILE REFERENCE: 10147-14
; CURRENT APPLICATION NUMBER: US/09/411,132A
; CURRENT FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-411-132A-2
Alignment Scores: 1.84e-45 Length: 1401
Score: 461.50 Matches: 129
Percent Similarity: 46.57% Conservative: 68
Best Local Similarity: 30.50% Mismatches: 173
Query Match: 19.35% Indels: 53
Gaps: 14
DB: 4
US-10-019-341-3 (1-448) x US-09-411-132A-2 (1-1401)
QY 5 ArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGluAspThrAlaGlu 24
Db 105 CAGGACTTCTCAACAGAGTTGGTAGTTTACCTGGTCTCCAGAGAGAGATAAA----- 158
QY 25 AspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys----- 40
Db 159 -----CACTCGTTTCTCTCTACACTATACAAATCCCAATGCCTATCAGGAGAT 209
QY 41 -----HisPheAsnHisSerSer-LysThrPhe----- 49
Db 210 CAGTGGGTAAATCTTCACTATCCAGCCTCATATTTTGGAAACAGACAGATCACCCG 269
QY 50 -MetValIleHisGlyThrValThrGlyMetTyrGluSerTyrValProLysLeuVa 69
Db 270 TATCAACATAGCTGGATGGAAACACAGATGGC-----AAATGGCAGAGACATGTG 320
QY 69 lAlaAlaLeuTyrLysArgGluProAspSerAsnValIleValValAspThrLeuSerAr 89
Db 321 CAATGTGTGTCTACAGCTGAA---GATATAAATTCATTAAATTTAGATTGGATCAACGG 377
QY 89 gAlaGlnGluHisTyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAl 109
Db 378 TTCACGGGAA---TACATCCATGCTGTAACAATCTCCGTGTGTGTGTGTGTGTGTGTGT 434
QY 109 aArgPheIleAsnTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLe 129
Db 435 TTATTTTATGATGTTCTCATGAAATAATTTGAATATTCCTCTCTAAAGTGCACCTTGT 494
QY 129 uGlyTyrSerIleuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysLysVa 149
Db 495 TGGCCACAGCTTGGGACACACCTGGCTGGGGAGCTGGGTTCAGGATA---CCAGGCT 551
QY 149 lAsnArgIleThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSe 169
Db 552 TGGAAAGATTAAGTGGGTGGACCCAGCTGGGCCATTTTTCACAACTCCCAAGGAAGT 611

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QY 169 rArgLeuSerProAspAlaAspPheValAspValLeuHisThr----- 184
Db 612 CAGGCTAGACCCCTCGGATGCCAACTTTGTGAGTTATTCATACAAATCGACTCGCAT 671
QY 185 ----PheThrArgGlySerProGlyArgSerIleGlyLeuGlnYsProValGlyHisVa 203
Db 672 CCTCTTTGAGCTTGGT-----GTTGGAACCATTCGATCTGTGTGTCATCT 716
QY 203 lAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsn-----IleGlyGluAl 221
Db 717 TGACTTTTACCACAAATGGAGGAGACACATGCCAGGATGTGAAGACTTAATACACCTTT 776
QY 221 alleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSerHi 241
Db 777 ACTGAATTTAACTTCAATGCTTTACAAAAAGAAATGGCTTCCTCTTTGACTGTAACCA 836
QY 241 sGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLysAl 261
Db 837 TGCCCGAAGTTATCAATTTATGCTGAAAGCAATCTTAATCCTGAT---GCATTTATTGTC 893
QY 261 aTyrArgCysSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLysAs 281
Db 894 TTATCCTTGTAGATCCTACACATCTTTAAAGCAGGAAATGCTCTTTTGTTCAAAGA 953
QY 281 nArgCysAsnAnLeuGlyTyrGluIleAsnLysValArgAlaLys-----Ar 297
Db 954 AGGTGCCCCAACAAATGGGTCAATTTGCTGATAGATTTCATTTCAAAAATATGAAGACTAA 1013
QY 297 sSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGl 317
Db 1014 TGGATCAATATTTTAAACACAGGGTCCCTTTCCCATTTGCCCTTGGAGGACAA 1073
QY 317 nValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluI 337
Db 1074 ATTGCTCTTAAACTCAGTGGAGCGAAGTC-----ACTCAAGGAACCTGCTTTCT 1124
QY 337 eSerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSe 357
Db 1125 TCGTGTAGCGGGGCAATTTGGGAAACCTGGGAGTTTCCCATTTGTCAGTGGAAACTTGA 1184
QY 357 rThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuMe 377
Db 1185 GCCAGGCATGACTTACACAAATTAATCGATGCGAGAGTTAAGTTGGAACATTAACAAG 1244
QY 377 tLeuLysLeuLysTyrLys-----SerAspSerTyr-PheSerTyrSerAspT 393
Db 1245 TGTTCACTTCATCTGGAAAAACATTTCTTTGAAGATTTCTCAGAATAAGTTGGGAGAGA 1304
QY 393 rpTTP 394
Db 1305 AATGG 1309

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RESULT 9

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US-09-411-132A-1
; Sequence 1, Application US/09411132A
; Patent No. 6558936
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: No. 6558936el Human Lipase Proteins, Nucleic Acides Encoding
; TITLE OF INVENTION: Them, and Uses of Both of These
; FILE REFERENCE: 10147-14
; CURRENT APPLICATION NUMBER: US/09/411.132A
; CURRENT FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2352
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (2159)

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; NAME/KEY: unsure
; LOCATION: (2307)
; NAME/KEY: unsure
; LOCATION: (2313)
US-09-411-132A-1

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Alignment Scores:

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Pred. No.: 4,48e-45 Length: 2352
Score: 461.50 Matches: 129
Percent Similarity: 46.57% Conservative: 68
Best Local Similarity: 30.50% Mismatches: 173
Query Match: 19.35% Indels: 53
DB: 4 Gaps: 14

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US-10-019-341-3 (1-448) x US-09-411-132A-1 (1-2352)

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QY 5 ArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGluAspThrAlaGlu 24
Db 229 CAGGACTTTCTCAACAGAGTTGGTAGGTTTACCTGCTCCAGAGAGATAAAA----- 282
QY 25 AspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys----- 40
Db 283 -----CACTCGTTTCTCTCTACACTATACAAATCCCAATGCCTATCAGGAGAT 333
QY 41 -----HisPheAsnHisSerSer-LysThrPhe----- 49
Db 334 CAGTCGGGTTAATTTCTCAACTATCCAAAGCCTCATATTTTGGNACAGACAGATCACCG 393
QY 50 -MetValIleHisGlyTyrThrValThrGlyMetTyrGluSerTyrValProLysLeuVa 69
Db 394 TATCAACATAGCTGATGGAAGAACAGATGGC-----AAATGGCAGAGACATGTG 444
QY 69 lAlaAlaLeuTyrLysArgGluProAspSerAsnValIleValValAspTyrLeuSerAr 89
Db 445 CAATGTGTGTACAGCTGGAA--GATATAAATTCGCAATTAATTAGATTGGATCAACGG 501
QY 89 gAlaGlnGluHisTyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAl 109
Db 502 TTCACGGGAA---TACATCCATGCTGTAACAATCTCGTGTGTGTGTGTGTGTGTGTGTGT 558
QY 109 aArgPheIleAsnTyrMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLe 129
Db 559 TTATTTTATTGATGTTCTCATGAAAAAATTTGAATATTTCCCTCTTAAAGTGCATTCAT 618
QY 129 uGlyTyrSerLeuGlyAlaHisAlaGlyIleAlaGlySerLeuThrAsnLysLysVa 149
Db 619 TGGCCACAGCTTGGGAGCACACCTGGCTGGGAGAGCTGGGTCAAGGATA---CCAGGCCT 675
QY 149 lAsnArgIleThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProse 169
Db 676 TGGAGAATAAATCTGGGTGGAGCCAGCTGGGCCATTTTCCACAACACTCCAAAGGAAGT 735
QY 169 rArgLeuSerProAspAlaAspPheValAspValLeuHisThr----- 184
Db 736 CAGGTAGACCCCTCGGATGCCAACTTTGTGACGTTATTATACATAAATGCAGCTCGCAT 795
QY 185 ----PheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProValGlyHisVa 203
Db 796 CCTCTTTGAGCTTGGT-----GTTGGAACCATTCGATCTGTGTGTCATCT 840
QY 203 lAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsn-----IleGlyGluAl 221
Db 841 TGACTTTTACCACAAATGGAGGAGACACATGCCAGGATGTGAAGACTTAATACACCTTT 900
QY 221 alleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSerHi 241
Db 901 ACTGAATTTAACTTCAATGCTTTACAAAAAGAAATGGCTTCCTCTTTGACTGTAACCA 960
QY 241 sGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLysAl 261
Db 961 TGCCCGAAGTTATCAATTTTATGCTGAAAGCAATCTTAATCCTGAT---GCATTTATTGTC 1017
QY 261 aTyrArgCysSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLysAs 281

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Mon Oct 25 15:42:53 2004

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; NAME/KEY: UNSURE
; LOCATION: 305
; OTHER INFORMATION: Xaa-Pro or Thr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 376
; OTHER INFORMATION: Xaa= * or Gly
US-09-513-999C-79

Alignment Scores:
Pred. No.: 2,3e-44 Length: 1206
Score: 451.50 Matches: 108
Percent Similarity: 49.71% Conservative: 64
Best Local Similarity: 31.21% Mismatches: 155
Query Match: 18.93% Indels: 19
DB: 4 Gaps: 9

US-10-019-341-3 (1-448) x US-09-513-999C-79 (1-1206)
Qy 9 AspIleGluSerLysPheAlaLeuArgThrProGluAspThrAlaGluAspThrCysHis 28
Db 177 GATGTCACACCCCGCTTCTCTATATATAATGAGAAC-----CCAAACAACATTTCAA 230
Qy 29 LeuIleProGlyValAlaGluSerValAlaThrCysHisPheAsnHisSerSerLysThr 48
Db 231 GAAGTTGGCGGAGATTTCATCAAGCATCAGTGGCTCCAAATTTCAAACAACAAATAGAAAACT 290
Qy 49 PheMetValIleHisGlyTrpThrValThrGlyMetTyrGluSerTrpValProLysLeu 68
Db 291 CGCTTTTATTATTCGA-----TTCATAGACAGGAGGAGAGAAACTGGCTGCCCAATGG 344
Qy 69 ValAlaAlaLeuTyrLysArgGluProAspSerAsnValIleValValAspTrpLeuSer 88
Db 345 TCAAGAAATCTGTTCAAGGTGGA---AGTGGAACCTGTATCTGTGTGACTGGAAAGGT 401
Qy 89 ArgAlaGlnGluHisTyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspVal 108
Db 402 GGCTCCGAACTGGATACACACAAGCTCGCAGAACATCAGGATCGTGGAGCAGAGAGTG 451
Qy 109 AlaArgPheIleAsnTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeu 128
Db 462 GCATATTTTGTGAATTTCTTCAGTCGGCGTTCGGTTACTCACCITCCAAATGGCATGTC 521
Qy 129 LeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysLys 148
Db 522 ATTGGCCACAGCTGGTGGTCCACACGCTGCTGGGGAGGCTGGAAGAGAGAACCAATGGGACC 581
Qy 149 ValAsnArgIleThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaPro 168
Db 582 ATTGGACGCATCACAGGGTTGGACCCAGCAGAACCTTGCTTTTCAGGGCACACCTGTAATTA 641
Qy 169 SerArgLeuSerProAspAspAlaAspPheValAspValLeuHisThrPheThrArgGly 188
Db 642 GTCCGATTGGACCCAGCGATGCCAAATTTGTGGATGTAATTCAC-----ACGGATGGT 695
Qy 189 Ser-----ProGlyArgSerIleGlyIleGlnLysProValGlyHisValAspIle 205
Db 696 GCGCCCATAGTCCCAATTTGGGGTTTGAATGAGCAAGTCGTGGGCCACCTAGATATTC 755
Qy 206 TyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGluAlaIleArgValIle 225
Db 756 TTTCCTCAATGGAGAGTGGAAATGCCCTGGATGTAAAAAGAACATCTCTCTCAGATTGTG 815
Qy 226 AlaGluArgGlyLeuGlyAsp---ValAspGlnLeuValLysCysSerHisGluArgSer 244
Db 816 GACATAGACGAATCTGGGAGGAGGACTCGAGACTTTTGGCGCTGTATCTACTTAAAGAAGC 875
Qy 245 IleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLysAlaTyrArgCys 264
Db 876 TACAAATATTACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 932
Qy 265 SerSerLysGluAlaPheGluLysGlyLeuSerCysArgLysAsnArgCysAsn 284

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; NAME/KEY: UNSURE
; LOCATION: 305
; OTHER INFORMATION: Xaa-Pro or Thr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 376
; OTHER INFORMATION: Xaa= * or Gly
US-09-513-999C-79

Alignment Scores:
Pred. No.: 2,3e-44 Length: 1206
Score: 451.50 Matches: 108
Percent Similarity: 49.71% Conservative: 64
Best Local Similarity: 31.21% Mismatches: 155
Query Match: 18.93% Indels: 19
DB: 4 Gaps: 9

US-10-019-341-3 (1-448) x US-09-513-999C-79 (1-1206)
Qy 9 AspIleGluSerLysPheAlaLeuArgThrProGluAspThrAlaGluAspThrCysHis 28
Db 177 GATGTCACACCCCGCTTCTCTATATATAATGAGAAC-----CCAAACAACATTTCAA 230
Qy 29 LeuIleProGlyValAlaGluSerValAlaThrCysHisPheAsnHisSerSerLysThr 48
Db 231 GAAGTTGGCGGAGATTTCATCAAGCATCAGTGGCTCCAAATTTCAAACAACAAATAGAAAACT 290
Qy 49 PheMetValIleHisGlyTrpThrValThrGlyMetTyrGluSerTrpValProLysLeu 68
Db 291 CGCTTTTATTATTCGA-----TTCATAGACAGGAGGAGAGAAACTGGCTGCCCAATGG 344
Qy 69 ValAlaAlaLeuTyrLysArgGluProAspSerAsnValIleValValAspTrpLeuSer 88
Db 345 TCAAGAAATCTGTTCAAGGTGGA---AGTGGAACCTGTATCTGTGTGACTGGAAAGGT 401
Qy 89 ArgAlaGlnGluHisTyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspVal 108
Db 402 GGCTCCGAACTGGATACACACAAGCTCGCAGAACATCAGGATCGTGGAGCAGAGAGTG 451
Qy 109 AlaArgPheIleAsnTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeu 128
Db 462 GCATATTTTGTGAATTTCTTCAGTCGGCGTTCGGTTACTCACCITCCAAATGGCATGTC 521
Qy 129 LeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysLys 148
Db 522 ATTGGCCACAGCTGGTGGTCCACACGCTGCTGGGGAGGCTGGAAGAGAGAACCAATGGGACC 581
Qy 149 ValAsnArgIleThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaPro 168
Db 582 ATTGGACGCATCACAGGGTTGGACCCAGCAGAACCTTGCTTTTCAGGGCACACCTGTAATTA 641
Qy 169 SerArgLeuSerProAspAspAlaAspPheValAspValLeuHisThrPheThrArgGly 188
Db 642 GTCCGATTGGACCCAGCGATGCCAAATTTGTGGATGTAATTCAC-----ACGGATGGT 695
Qy 189 Ser-----ProGlyArgSerIleGlyIleGlnLysProValGlyHisValAspIle 205
Db 696 GCGCCCATAGTCCCAATTTGGGGTTTGAATGAGCAAGTCGTGGGCCACCTAGATATTC 755
Qy 206 TyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGluAlaIleArgValIle 225
Db 756 TTTCCTCAATGGAGAGTGGAAATGCCCTGGATGTAAAAAGAACATCTCTCTCAGATTGTG 815
Qy 226 AlaGluArgGlyLeuGlyAsp---ValAspGlnLeuValLysCysSerHisGluArgSer 244
Db 816 GACATAGACGAATCTGGGAGGAGGACTCGAGACTTTTGGCGCTGTATCTACTTAAAGAAGC 875
Qy 245 IleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLysAlaTyrArgCys 264
Db 876 TACAAATATTACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 932
Qy 265 SerSerLysGluAlaPheGluLysGlyLeuSerCysArgLysAsnArgCysAsn 284

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| | | | | |
|------|-----------------------------|--------------------------|--------------------|------|
| 933 | GCCTCTTACAAAGCTTCTAC | CTGCAAAACAAGTGTTCCTCTG | CTCAAGTGAGGCTGCMCA | 992 |
| 285 | AsnLeuGlyTyrGluIleAsnLysVal | ArgAlaLysArgSer | -----SerLysMet | 301 |
| 993 | CAGATGGTCTACTATGCTGATAG | TATCTCGGAAACAATATGATGG | GGCCCAAAATTT | 1052 |
| 302 | TyrLeuLysThrArgSerGlnMet | ProTyrLysValPheHisTyrGln | ValLysIleHis | 321 |
| 1053 | TATCTAGACACTGGTGTATGCG | CAGTAATTTTTCGAGGTATAGG | TATCTGTCACA | 1112 |
| 322 | PheSerGlyThrGluSerGluThr | HisThrAsnGlnAlaPheGluIle | SerLeuTyrGly | 341 |
| 1113 | CTGCTCGAAAAAGGTTACAG | ACAC-----ATACTAGTTTCT | TTTGTTCGGA | 1160 |
| 342 | ThrValAlaGluSerGlu | 347 | | |
| 1161 | AATAAAGGAACCTCTAAG | 1178 | | |

RESULT 11

US-08-905-124-4
 ; Sequence 4, Application US/08905124
 ; Patent No. 6074825
 ; GENERAL INFORMATION:
 ; APPLICANT: Rundell, Clark A.
 ; APPLICANT: Vary, Calvin P.H.
 ; TITLE OF INVENTION: STABLE ENCAPSULATED REFERENCE
 ; TITLE OF INVENTION: NUCLEIC ACID AND METHOD OF MAKING
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wood, Herron & Evans, L.L.P.
 ; STREET: 2700 Carew Tower
 ; CITY: Cincinnati
 ; STATE: OH
 ; COUNTRY: USA
 ; ZIP: 45202-2917
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows DEMONSTRATION Version 2.0.D
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/905,124
 ; FILING DATE: 31-JUL-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Frei, Donald F
 ; REGISTRATION NUMBER: 21,190
 ; REFERENCE/DOCKET NUMBER: CASI-02
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 513-241-2324
 ; TELEFAX: 513-421-7269
 ; TELEEX:

| | |
|---------------------|----------|
| Alignment Scores: | |
| Pred. No.: | 4.63e-41 |
| Score: | 414.00 |
| Percent Similarity: | 100.00% |
| Length: | 231 |
| Matches: | 77 |
| Conservative: | 0 |

| | | | | |
|---|---------|--|-------------|---|
| Best Local Similarity: | 100.00% | | Mismatches: | 0 |
| Query Match: | 17.36% | | Indels: | 0 |
| DB: | 3 | | Gaps: | 0 |
| US-10-019-341-3 (1-448) x US-08-905-124-4 (1-231) | | | | |
| QY | 154 | GlyLeuAspProAlaGlyProAsnPhcIuTyrrAlaGluAlaProSerArgLeuSerPro | 173 | |
| Db | 1 | GGCTTCGATCCAGCTGGACCTTAACCTTTGAGTATGCAGAAGCCCGAGTCGTCTTCTCCT | 60 | |
| QY | 174 | AspAspAlaAspPheValAspValLeuHisThrPheThrArgGlySerProGlyArgSer | 193 | |
| Db | 61 | GATGATGCAGATTTTGTAGAGCTCTTACACACATTCCACGAGGTCCTCCCTGGTCGAGAC | 120 | |
| QY | 194 | IleGlyIleGlnLysProValGlyHisValAspIleTyrrProAsnGlyGlyThrPheGln | 213 | |
| Db | 121 | ATTGGAAATCCAGAAACCATGTGGCAGATTGTGACATTTACCCGAATGGAGGTACTTTTCAG | 180 | |
| QY | 214 | ProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeu | 230 | |
| Db | 181 | CCAGGATGTAACTTTGAGAAGCTATCCGGCTGATTCAGACAGAGACATTT | 231 | |

RESULT 12

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US-09-799-451-90
; Sequence 90, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyang
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yungqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 90
; LENGTH: 1889
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (366)..(1334)
US-09-799-451-90

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| | | |
|------------------------|----------|------------------|
| Alignment Scores: | | |
| Pred. No.: | 2.54e-33 | Length: 1889 |
| Score: | 363.00 | Matches: 101 |
| Percent Similarity: | 42.98% | Conservative: 46 |
| Best Local Similarity: | 29.53% | Mismatches: 89 |
| Query Match: | 15.22% | Indels: 106 |
| DB: | 4 | Gaps: 13 |

US-10-019-341-3 (1-448) x US-09-799-451-90 (1-1889)

QY

111 PheIleAsnTrpMetGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGly 130
|||||:: |||| |||| |

Mon Oct 25 15:42:53 2004

Patent No. 5593877
 GENERAL INFORMATION:
 APPLICANT: King, Te-Biao
 TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
 TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
 TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED
 TITLE OF INVENTION: THEREON
 NUMBER OF SEQUENCES: 62
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Klauber & Jackson
 STREET: 411 Hackensack Avenue
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/180,209B
 FILING DATE: 11-JAN-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/031,400
 FILING DATE: 11-MAR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-074 CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 487-5800
 TELEFAX: 201 343-1684
 TELEX: 133521
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1050 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..951
 US-10-019-341-3 (1-448) x US-08-180-209B-16 (1-1050)

Db 381 TTTATTACACAGATGTTGGCAGAA--GGAGCTTCTCTTGATGACATTTACATGATCGGA 437
 QY 131 TyrSerLeuGlyAlaHisAlaAlaGlySerLeuThrAsnLysLysValAsn 150
 Db 438 GTAAGTCTAGAGCCCAACATATCTGGTGTGGAGAGATGTACGATGCTGGG 497
 QY 151 ArgIleThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArg 170
 Db 498 AGAATTACAGCCCTCGACCTCGAGGCCCTTTATTCAACGGAGAACTCCACACAGACGA 557
 QY 171 LeuSerProAspAlaAspPheValAspValLeuHisThrPheThrArgGlySerPro 190
 Db 558 TTAGATCCCACTGATGCGACGTTGTGTGATGTCATCCATTCGACACT----- 605
 QY 191 GlyArgSerIleGlyIleGlnLysProValGlyHisValAspIleTyrProAsnGlyGly 210
 Db 606 ---GATGCACCTGGGTACAGAGCCATAGAACATAGACTTCTACCCAAATGGAGGA 662
 QY 211 ThrPheGlnProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeu 230
 Db 663 TTGGATCAACCTGGCTGC-----CCCAAAACAATATTG 695
 QY 231 GlyAspValAspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAsp 250
 Db 696 GGAGGATTT---CAGTATTTAAATGTGACACCCAGAGTCTGTATACCTGTACCTGTCT 752
 QY 251 SerLeuLeuAsnGluGluAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPhe 270
 Db 753 TCC---CTGAGAGAGAGTGCACCATCATCTGGTATCCCTGTGACTCTCCACGAGATTAT 809
 QY 271 GluLysGlyLeuCysLeuSerCys-----ArgLysAsnArgCysAsnAsnLeuGly 287
 Db 810 AGGAATGGCACTGTGTGCTGCTGCGGACGTCACAAAAGAGTCTCTCCCTTTCTGGGC 869
 QY 288 TyrGluIleAsnLys-----ValArgAlaLys-----ArgSerSerLysMet 301
 Db 870 TATTATGCTGATAATTGGAAAGACCATCTAAGGGGGAAGATCCTCCATGACGAGGCA 929
 QY 302 TyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIleHis 321
 Db 930 TTCTTTGACACAGCTGAGGAGACCCATCTGCGATGATCATTTCTGTGGATATT--- 986
 QY 322 PheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyrGly 341
 Db 986 ----- 986
 QY 342 ThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLysThr 361
 Db 987 -----ATAACATGGAACAG--- 1001
 QY 362 TyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLys 381
 Db 1002 -----AATGTAAGAAGAGGGGACATTACCATC----- 1028
 QY 382 TrpLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerProGlyPheAlaIle 401
 Db 1028 ----- 1028
 QY 402 GlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArgGlu 421
 Db 1029 ---AAATTGAGAGCAAGCTGGAAACACC-----ACAGATCC 1064
 QY 422 LysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAspLys 441
 Db 1065 AAATCAATCAT-----GAACCCCAACCATTTTCAAGAAATATCAACCAAGTG 1109
 QY 442 SerLeu 443
 Db 1110 AGTCTA 1115
 RESULT 13
 US-08-180-209B-16
 ; Sequence 16, Application US/08180209B

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QY 113 nTrpMetGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSerLe 133
Db 405 GAAACTTGTAGAACAAATATAAGTCCGATGACAAATATACGATCTGGTGGACACAGTTT 464
QY 133 uGlyAlaHisAlaAlaGlyLeuGlySerLeuThrAsnLys-----LysVa 149
Db 465 GGGCGCACACATTCAGGTTTCGAGGCAAAAGAGTTCAAGAGTTAAATATTAGGAAATTT 524
QY 149 lAsnArgIleThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSe 169
Db 525 TTCTGAAATATTGGGCTTCTGCTGCTGGCCCTAGTTTCAAGAAATGATTGTTCCGA 584
QY 169 rArgLeuSerProAspAlaAspPheValAspValLeuHisThrPheThrArgGlySe 189
Db 585 GAGAATCTGGACAGACGACACATATGATGACAAATTTTACATACA-----630
QY 189 rProGlyArgSerIleGlyLeuGlnLysProValGlyHisValAspIleTyrProAsnGl 209
Db 631 ----TCAGCAATTTAGGAACAGAGAACTCTTGGCACCGCTGCTTACATAATAA 686
QY 209 yGlyThrPheGlnProGlyCysAsn-----IleGlyGluAlaIleArgValIleAlaGl 227
Db 687 CGGAAGTAATCAACCGGTTGCAGATATATTATGGAGAACT-----729
QY 227 uArgGlyLeuGlyAspValAspGlnLeuValLysCysSerHisGluArgSerIleHisLe 247
Db 730 ----TGCTCTCATACGAGCGCGTGAATA 755
QY 247 uPheIleAspSerLeuLeuAsnGlu-----GluAsnPr 258
Db 756 CTTTACCGAGTGCATAAGACGGCAATGTTGTTAAATTGGGTCGCCGAGTCCCAAGAAATCC 815
QY 258 sSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCy 278
Db 816 GCAGCGCTGTTTGAAGTGCACAGAAACGAGTGGCTTTCGTTGGATTAAACGCAAGAA 875
QY 278 sArgLysAsnArg-----CysAsnAs 285
Db 876 ATATCCTAAAGGGGCTCATTTTATGATACCGGTTGAAGCTGAAGCTCCATATTGCAATAA 935
QY 285 mLeuGlyTyr-----288
Db 936 CAACGGGAAATAATTTAATTATATAAAACAACTTACTATTGACAAAGTGCAATTTGT 995
QY 289 -----GluIleAsnLysValArgAlaLysArgSerSerLys 300
Db 996 TAATGATGAATGAATAAATACGATTCAAGAAAAAATAA 1038

RESULT 14
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; Sequence 16, Application US/08385745
; Patent No. 5612209
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; TITLE OF INVENTION: Cloning and Recombinant Production of
; TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies
; TITLE OF INVENTION: Based Thereon
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,745
; FILING DATE:
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/031,400
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 3288-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1050 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..951
; US-08-385-745-16
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Pred. No.: 1.38e-29 Length: 1050
Score: 328.50 Matches: 87
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Best Local Similarity: 27.62% Mismatches: 96
Query Match: 13.77% Indels: 82
DB: 1 Gaps: 10
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US-10-019-341-3 (1-448) x US-08-385-745-16 (1-1050)

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QY 62 uSerTrpValProLysLeuValAlaLeuTyrLysArgGluProAspSerAsnValIl 82
Db 231 AAATTCCTGTTGCTATGTCAGAGGCTCTTATGCAT-----ACAGTGATTTTCTTATAAT 284
QY 82 eValValAspTrp---LeuSerArgAlaGlnGluHisTyrPro-----95
Db 285 TATGTCGATTGGCGGATGGCTGCTGTTACTGTAATACCGAGTCTGAAGTATATGTT 344
QY 96 -----ValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAlaArgPheIleAs 113
Db 345 TTATAAGGCTGCCGTTGGTAATACACGCTTAGTTGGAAATTTTATCGCTATGATCGCAA 404
QY 113 nTrpMetGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSerLe 133
Db 405 GAAACTTGTAGAACAAATATAAGTCCGATGACAAATATACGATCTGGTGGACACAGTTT 464
QY 133 uGlyAlaHisAlaAlaGlyLeuGlySerLeuThrAsnLys-----LysVa 149
Db 465 GGGCGCACACATTCAGGTTTCGAGGCAAAAGAGTTCAAGAGTTAAATATTAGGAAATTT 524
QY 149 lAsnArgIleThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSe 169
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QY 169 rArgLeuSerProAspAlaAspPheValAspValLeuHisThrPheThrArgGlySe 189
Db 585 GAGAATCTGGACAGACGACACATATGATGACAAATTTTACATACA-----630
QY 189 rProGlyArgSerIleGlyLeuGlnLysProValGlyHisValAspIleTyrProAsnGl 209
Db 631 ----TCAGCAATTTAGGAACAGAGAACTCTTGGCACCGCTGCTTACATAATAA 686
QY 209 yGlyThrPheGlnProGlyCysAsn-----IleGlyGluAlaIleArgValIleAlaGl 227
Db 687 CGGAAGTAATCAACCGGTTGCAGATATATTATGGAGAACT-----729
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QY 227 uArgGlyLeuGlyAspValaspGlnLeuValLysCysSerHisGluArgSerIleHisLe 247
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QY 247 uPheileAspSerLeuLeuAanglu-----GluAsnPr 258
Db 756 CTTTACCGAGTGCATAAGACGGAATGTTGTTAATTGGGTCGCCGACGTCCAAGAATCC 815
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QY 278 sArgLysAsnArg-----CysAsnAs 285
Db 876 ATATCCTAAAGGGCTCATTTTATGTACCGGTTGAAGCTGAAGCTCCATATGCAATAA 935
QY 285 nLeuGlyTyr----- 288
Db 936 CAACGGGAAATPAATTTAATTATATAAAAAAACATTACTATTGACACAAAGTGCAATTGT 995
QY 289 -----GluLeuAsnLysValArgAlaLysArgSerSerLys 300
Db 996 TAAATGATGAATGAATAAATTCAGATTCAAGAAAAAATAA 1038
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US-08-485-388-16
; Sequence 16, Application US/08485388
; Patent No. 6270763
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; TITLE OF INVENTION: Cloning and Recombinant Production of
; TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies
; TITLE OF INVENTION: Based Thereon
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,388
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/385,745
; FILING DATE: 08-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/031,400
; FILING DATE: 11-MAR-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-074 FWCA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5900
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1050 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
US-08-485-388-16
Alignment Scores:
Pred. No.: 1,38e-29 Length: 1050
Score: 328.50 Matches: 87
Percent Similarity: 43.49% Conservative: 50
Best Local Similarity: 27.62% Mismatches: 96
Query Match: 13.77% Indels: 82
DB: 3 Gaps: 10
US-10-019-341-3 (1-448) x US-08-485-388-16 (1-1050)
QY 43 AsnHisSerSerLysThr-PheMetValIleHisGlyTrpThrValThrGlyMetTyrGl 62
Db 171 AATCATAAACGTCACAGTTGTATTACATACGATGGTTTACTCTGCTGACACGAA 230
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QY 113 nTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSerLe 133
Db 405 GAACTTGTAGAACATATATAAGTCCGATGACAAATATACGACTCGTGGGACACAGTTT 464
QY 133 uGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLys-----LysVa 149
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QY 149 lAsnArgIleThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSe 169
Db 525 TTCTGAAATTAATTGGGCTTATCTCTGCTGGGCTAGTTTTCAGAAAAATGATTTGCCGA 584
QY 169 rArgLeuSerProAspAlaAspPheValAspValLeuHisThrPheThrArgGlySe 189
Db 585 GAGAACTCGCAGACAGACACCATATGTACAAATTTTACATACA----- 630
QY 189 rProGlyArgSerIleGlyIleGlnLysProValGlyHisValAspIleTyrProAsnGl 209
Db 631 ----TCGAGCAATTTAGGAACAGAGAGAACTCTTGGCAGCGTCGATTTCTACATAATAA 686
QY 209 yGlyThrPheGlnProGlyCysAsn-----IleGlyGluAlaIleArgValIleAlaGl 227
Db 687 CGGAAGTAATCAACCCGGTTGCAGATATATTATGGAGAACT----- 729
QY 227 uArgGlyLeuGlyAspValaspGlnLeuValLysCysSerHisGluArgSerIleHisLe 247
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Search completed: October 24, 2004, 21:13:34
Job time : 143 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 18:24:55 ; Search time 678 Seconds
(without alignments)

3385.718 Million cell updates/sec

Title: US-10-019-341-3

Perfect score: 2385

Sequence: 1 ADQRDFIDIESKFAALRTP.....GRAPAVFKCHDKSLNKGK 448

Scoring table: BLOSUM62

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Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 3407233 seqs, 2561960514 residues

Total number of hits satisfying chosen parameters: 6814466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA -OPMT=fastap -SUFFIX=rnpb -MINMATCH=0.1

-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62

-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100

-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0

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6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*

7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*

9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*

10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*

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21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 2385 | 100.0 | 3549 | 9 | US-09-954-456-2217 |
| 2 | 2385 | 100.0 | 3549 | 10 | US-09-802-640-13 |
| 3 | 2385 | 100.0 | 3549 | 15 | US-10-403-902A-13 |
| 4 | 2385 | 100.0 | 3549 | 17 | US-10-755-889-99 |
| 5 | 2378 | 99.7 | 3635 | 14 | US-10-116-802-28 |
| 6 | 2372 | 99.5 | 4075 | 10 | US-09-971-392-107 |
| 7 | 2235.5 | 93.7 | 3617 | 16 | US-10-388-934-188 |
| 8 | 1161 | 48.7 | 2565 | 15 | US-10-128-449A-7 |
| 9 | 1161 | 48.7 | 3927 | 15 | US-10-354-358-45 |
| 10 | 1161 | 48.7 | 3927 | 15 | US-10-172-118-1234 |
| 11 | 1161 | 48.7 | 3927 | 16 | US-10-211-462-228 |
| 12 | 1161 | 48.7 | 3927 | 17 | US-10-342-887-1234 |
| 13 | 1161 | 48.7 | 3927 | 17 | US-10-319-915-4 |
| 14 | 1161 | 48.7 | 4315 | 15 | US-10-133-013-213 |
| 15 | 1158 | 48.6 | 2227 | 17 | US-10-319-915-99 |
| 16 | 1157 | 48.5 | 3610 | 17 | US-10-319-915-11 |
| 17 | 1038 | 43.5 | 1603 | 10 | US-09-802-640-19 |
| 18 | 1038 | 43.5 | 1603 | 15 | US-10-403-902A-19 |
| 19 | 1014.5 | 42.5 | 1605 | 9 | US-09-917-800A-1549 |
| 20 | 952 | 40.3 | 1323 | 16 | US-10-210-130-89 |
| 21 | 928 | 38.9 | 1035 | 15 | US-10-128-449A-9 |
| 22 | 928 | 38.9 | 1065 | 15 | US-10-128-449A-5 |
| 23 | 928 | 38.9 | 1382 | 15 | US-10-128-449A-3 |
| 24 | 928 | 38.9 | 1510 | 9 | US-09-978-295A-177 |
| 25 | 928 | 38.9 | 1510 | 9 | US-09-978-697-177 |
| 26 | 928 | 38.9 | 1510 | 9 | US-09-978-192A-177 |
| 27 | 928 | 38.9 | 1510 | 9 | US-09-999-832A-177 |
| 28 | 928 | 38.9 | 1510 | 10 | US-09-978-189-177 |
| 29 | 928 | 38.9 | 1510 | 10 | US-09-978-608A-177 |
| 30 | 928 | 38.9 | 1510 | 10 | US-09-978-585A-177 |
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| 35 | 928 | 38.9 | 1510 | 10 | US-09-981-915A-177 |
| 36 | 928 | 38.9 | 1510 | 10 | US-09-978-824-177 |
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| 38 | 928 | 38.9 | 1510 | 10 | US-09-999-834A-177 |
| 39 | 928 | 38.9 | 1510 | 10 | US-09-978-423A-177 |
| 40 | 928 | 38.9 | 1510 | 10 | US-09-978-193A-177 |
| 41 | 928 | 38.9 | 1510 | 10 | US-09-999-830A-177 |
| 42 | 928 | 38.9 | 1510 | 10 | US-09-978-757A-177 |
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| 44 | 928 | 38.9 | 1510 | 10 | US-09-978-643A-177 |
| 45 | 928 | 38.9 | 1510 | 10 | US-09-978-775A-177 |

ALIGNMENTS

RESULT 1

US-09-954-456-2217
; Sequence 2217, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Can
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR FILING DATE: 2000-09-18
; PRIOR FILING DATE: 2000-09-18
; PRIOR FILING DATE: 2000-09-20
; PRIOR FILING DATE: 2000-09-25
; PRIOR FILING DATE: 2000-09-25
; PRIOR FILING DATE: 2000-09-25
; PRIOR FILING DATE: 2000-09-25
; PRIOR FILING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2217
LENGTH: 3549
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-2217

Alignment Scores:
Pred. No.: 5,18e-277 Length: 3549
Score: 2385.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-019-341-3 (1-448) x US-09-954-456-2217 (1-3549)

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DB 256 GCGGACCAAGAAGAGATTTCGACATCGAAGATGAATTTGCCCTAAGGACCCCTGAA 315
QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
DB 316 GACACAGCTGAGGACACTTGGCCACTCATTCGCGAGTAGCAGAGTCCGTGCTACCTGT 375
QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTrpThrValThrGlyMet 60
DB 376 CATTTCAATCACAGCAGCAAAACCTTCATGTTGATCCATCGCTGGAGCGGTAAACAGGAATG 435
QY 61 TyrGluSerTrpValProLysLeuValAlaLeuTyrLysArgGluProAspSerAsn 80
DB 436 TAGGAGATTGGTGCCAAACCTTGTGGCCGCTGTACAGAGAGAACCCAGACTCCAAAT 495
QY 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
DB 496 GTCAATTGGTGGACTGGCTGTACAGGGCTCAGGAGCAATTTACCCAGTGTCCGCGGCTAC 555
QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120
DB 556 ACCAAACTGGTGACAGAGATGTGGCCCGTTTATCAACTGGATGGAGGAGGATTTAAC 615
QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyIle 140
DB 616 TACCCTTGACAAATGTCATCTCTGGGATACAGCTTGGAGCCCATGTGTGGCATT 675
QY 141 AlaGlySerLeuThrAsnLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
DB 676 GCAGGAATGTGACCAATAAGAAAGTCAACAGAATTTACTGGCCCTCGATCCAGCTGGACCT 735
QY 161 AspPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
DB 736 AACTTTGAGTATGAGAAGCCCGAGTCGTCTTCTCTGATGATGAGATTTTGTAGAC 795
QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
DB 796 GTCTTACACACTTACAGAGAGGTCCCTGTGCGAGCAATTTGAATCCAGAAACCAAGTT 855
QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
DB 856 GGGCATGTGACATTTACCCGAATGGAGGTACTTTTCAGCCAGGATGTAACATTTGGAGAA 915
QY 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240

DB 916 GCTATCCGGGTGATTGTCAGAGAGGACTTGGAGATGTGGACCACTAGTAGTGCCTCC 975
QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
DB 976 CACGAGCGCTCCATTCTCTTCATGACTCTCTGTGTAAGTAAGAAATCCAGTAAG 1035
QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
DB 1036 GCCTACAGTGCAGTTCCAGGAAGCCTTTGAGAAAGGCTCTGCTTGAGTTGTAGAAAG 1095
QY 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys 300
DB 1096 AACCGCTGCAACAATCTGGCTATGAGATCAATAAGTCAGAGCCAAAGAGACGACAAA 1155
QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
DB 1156 ATGTACCTGAAAGACTCGTTCAGATGCCCTCAAAAGTCTTCCATTACCAAGTAAGATT 1215
QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
DB 1216 CATTTTCTGGGACTGAGAGTGAAACCCATACCAATCAGGCCCTTTGAGATTTCTCTGTAT 1275
QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
DB 1276 GGCACCGTGGCGAGAGTGAGAACATCCCATCTCTGCTGAAAGTTTCCCAAAATAAG 1335
QY 361 ThrTyrSerPheLeuIleTyrThrGluValAlaPheIleGlyGluLeuMetLeuLysLeu 380
DB 1336 ACCTACTCTCTCTTAATTTACACAGAGGTAGATATTTGGAGAACTACTCATGTTGAAGCTC 1395
QY 381 LysTyrLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerSerProGlyPheAla 400
DB 1396 AAATGGAAGAGTGATTCATCTTACTGCTGAGACTGTGGAGCAGTCCCGGCTTCGCC 1455
QY 401 IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
DB 1456 ATTCAGAGATCAGAGTAAAGCAGGAGAGACTCAGAAAAAGGTGATCTTCTGTTCTAGG 1515
QY 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
DB 1516 GAGAAAGTGTCTCATTTTGCAGAAAGAAAGGACCTCCGGTATTTGTGAAATCCCATGAC 1575
QY 441 LysSerLeuAsnLysLysSerGly 448
DB 1576 AGTCTCTGAATAAGAGTCAGGC 1599

RESULT 2

US-09-802-640-13
Sequence 13, Application US/09802640
Publication No. US20030036057A1
GENERAL INFORMATION:
APPLICANT: Braun, Andreas
APPLICANT: Bonsal Aruna
APPLICANT: Kleyen Patrick
TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
FILE REFERENCE: 24736-2048
CURRENT APPLICATION NUMBER: US/09/802,640
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Fast-Seq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 3549
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (175)...(1602)
OTHER INFORMATION: Nucleotide sequence encoding lipoprotein lipase
OTHER INFORMATION: (LPL)
US-09-802-640-13

Alignment Scores:

Pred. No.: 5,18e-277 Length: 3549
 Score: 2385.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-10-019-341-3 (1-448) x US-09-802-640-13 (1-3549)

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QY 1 AlaAspGlnArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
Db 256 GCGAGCAAGAGAGATTTATCGACATCGAAGTAAATTTGCCCTAAGAGCCCTGAA 315

QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
Db 316 GACACAGCTGAGGACACTTGCACCTCATTTCCGGAGTAGCAGAGTCGCTGCTACCTGT 375

QY 41 HisPheAsnHisSerLysThrPheMetValIleHisGlyTyrThrValThrGlyMet 60
Db 376 CATTTCAATCACAGCAGCAAAACCTTCATGGTGATCCATGGCTGGAGCGGTACAGGAATG 435

QY 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80
Db 436 TATGAGAGTTGGTGCCAAACTTTGGCCGCCCTGTACAAGAGAGAACCCAGACTCCAAT 495

QY 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
Db 496 GTCAATGTGGTGGCTGTGTACGGGCTCAGGAGCATTCACCACTGTCCCGGGCTAC 555

QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120
Db 556 ACCAACTGGTGGGACAGATGTGCCCGTTTATCACTGATGGAGGAGAGTTTAC 615

QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaGlyIle 140
Db 616 TACCCTCTGGCAATGTCCATCTCTGGGATACAGCCTTGGAGCCATGCTGCTGGCAT 675

QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
Db 676 CGAGAGCTCTGACCAATAGNAAGTCAACAGAAATTTACTGGCCTCGATCCAGCTGGAGCT 735

QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
Db 736 AACTTTGAGTATGCAGAGCCCGAGTGTCTTCTCTGATGATGACATTTGTAGAC 795

QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
Db 796 GTCTTACACATTCACAGAGGGTCCCTCGTGGAGCATTTGGAATCCAGAAACCACTT 855

QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
Db 856 GGGCATGTGACATTTACCGAATGGAGGTACTTTTCAGCCAGGATGTAAATTTGGAGAA 915

QY 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
Db 916 GCTATCCGCGTGATTCGACAGAGAGGACTTGGAGATGTGGACAGCTAGTGAAGTGTCTCC 975

QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
Db 976 CACAGCGCTCCATTCATCTCTTCATGACTCTCTGTTGAATGAAGAAATCCAAAGTAAG 1035

QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
Db 1036 GCCTACAGGTGCAGTTCCAGAGAGCCCTTTGAGAAAGGGCTCTGCTTGTAGTGTAGAAAG 1095

QY 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys 300
Db 1096 AACCGCTGCAACAATCTGGGCTATGAGATCAATAAAGTCAGAGCCAAAGAGAGCAAA 1155

QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
Db 1156 ATGTACCTGAAGACTCGTTCTCAGATGCCCTACAAAGTCTTCCATTACCAAGTAAAGATT 1215

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QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
Db 1216 CAITTTTCTGGACTGAGAGTGAACCCATACCAATCAGCCCTTTGAGATTCTCTGTAT 1275

QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrThrLeuProGluValSerThrAsnLys 360
Db 1276 GGCACCGTGGCCGAGAGTGAGAACATCCCATTCACCTGCTGCCTGAAGTTTCCACAAATAAG 1335

QY 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyLeuLeuMetLeuLysLeu 380
Db 1336 ACCTACTCTTCTTAATTTACACAGAGGTAGATATTGGAGAACTACTCATGTTGAAGCTC 1395

QY 381 LysTrpLysSerAspSerTyrPheSerTrpSerAspTrpSerProGlyPheAla 400
Db 1396 AAATGGAAGAGTATTACATCTTAGCTGGTCAGACTGGTGGAGAGTCCCGGCTTCGCC 1455

QY 401 IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
Db 1456 ATTCAGAGATCAGAGTAAAGCAGGAGACTTCAGAAAAAGGTGATCTTCTGTTCTAGG 1515

QY 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
Db 1516 GAGAAAGTGTCTCATTTTCAGAAAGAAAGGACCCCTGCGGTATTGTGAAATGCCATGAC 1575

QY 441 LysSerLeuAsnLysLysSerGly 448
Db 1576 AAGTCTCTGAATAAGAAGTCAGGC 1599

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RESULT 3

US-10-403-902A-13
 ; Sequence 13, Application US/10403902A
 ; Publication No. US20030224418A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Braun, Andreas
 ; APPLICANT: Bansal, Aruna
 ; APPLICANT: Kiehn, Patrick
 ; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
 ; FILE REFERENCE: 24736-2048B
 ; CURRENT APPLICATION NUMBER: US/10/403,902A
 ; PRIOR FILING DATE: 2003-07-21
 ; PRIOR APPLICATION NUMBER: 09/802,640
 ; PRIOR FILING DATE: 2001-03-09
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13
 ; LENGTH: 3549
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (175)...(1602)
 ; OTHER INFORMATION: Nucleotide sequence encoding lipoprotein lipase
 ; OTHER INFORMATION: (LPL)
 US-10-403-902A-13

Alignment Scores:

Pred. No.: 5,18e-277 Length: 3549
 Score: 2385.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 15 Gaps: 0

US-10-019-341-3 (1-448) x US-10-403-902A-13 (1-3549)

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QY 1 AlaAspGlnArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
Db 256 GCGAGCAAGAGAGATTTATCGACATCGAAGTAAATTTGCCCTAAGAGCCCTGAA 315

QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40

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Db 316 GACACAGCTGAGGACACTTGCACCTCATTCCTCCGAGTAGCAGAGTCCGTGGCTACCTGT 375
 Qy 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTrpThrValThrGlyMet 60
 Db 376 CATTTCAATACACAGCAGCAAACTTCTGTGTGTATCATGCTGCGGTAAACAGGAATG 435
 Qy 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80
 Db 436 TATGAGAGTGGTGCCAAACTTGTGGCCGCTGTACAAAGAGAGAACCCAGACTCCCAAT 495
 Qy 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
 Db 496 GTCATTGTGTGGTGTGCTGCTGCGGCTCAGGAGCAATACCCAGTGTCCGCGGCTAC 555
 Qy 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120
 Db 556 ACCAAACTGGTGGGACAGAGTGTGGCCGGTTATCACTGGATGGAGGAGGTTTAAAC 615
 Qy 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaGlyTyr 140
 Db 616 TACCTCTGGACATGTCCATCTCTTGGATACAGCTTGGAGCCCATGCTCTGGCATT 675
 Qy 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
 Db 676 GCAGGAAGTCTGACCAATAAGAAAGTCAACAGAAATTAAGTGGCTGATCCAGCTGACCT 735
 Qy 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
 Db 736 AACTTTGATATGCAGAACCCCGAGTCTCTTCTCTGATGATGATGATGATGATGATGAT 795
 Qy 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
 Db 796 GTCTTACACATTCACAGAGGCTCCCTGTGTGAAGCATTTGGAATCCAGAAACCATGTT 855
 Qy 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
 Db 856 GGGCATGTGACATTTACCCGAATGAGGATGATTTTTCAGCCAGATGTAACATTTGAGAA 915
 Qy 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
 Db 916 GCTATCCGCTGTATGTCAGAGAGGAGCTTGGAGATGTGACAGCTAGTGAAGTGTCTCC 975
 Qy 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluLeuAsnProSerLys 260
 Db 976 CACGAGCGCTCCATTCATCTCTTCATCGACTCTCTGTGAATGAAGAAATCCAGTAAG 1035
 Qy 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
 Db 1036 GCCTACAGGTGCAGTTCAGAGGAGCCCTTTGAGAAAGGCTCTGCTTGTAGTGTAGAAAG 1095
 Qy 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys 300
 Db 1096 AACCGCTGCACAACTCTGGCTATGAGATCAATAAAGTCAGAGCCAAAGAGCAGCAAA 1155
 Qy 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
 Db 1156 ATGTACCTGAAGACTCGTCTCTCAGATGCCCTACAAAGCTTCCCAATTAAGTAAGATT 1215
 Qy 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
 Db 1216 CATTTTCTGGGACTGAGAGTGAACCCATACCAATCAGGCTTTGAGATTCTCTGTAT 1275
 Qy 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
 Db 1276 GGCACCGTGGCGGAGAGTGAACATCCATTCCTCTGCTGAAATTTCCACAAATAAG 1335
 Qy 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyLeuLeuMetLeuLysLeu 380
 Db 1336 ACCTACTCTCTTCTTAATTTACACAGAGTATGATTTGGAGAACTACTCATGTTGAGCTC 1395
 Qy 381 LysTrpLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerSerProGlyPheAla 400
 Db 1396 AAATGGAAAGAGTGAATTCATCTTTAGCTGTGCTCAGACTGCTGGAGCAGTCCCGGCTTCGCC 1455

Qy 401 IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
 Db 1456 ATTCAAGATCAGAGTAAAGCAGAGAGACTCAGAAAAAGGTGATCTTCTGTCTAGG 1515
 Qy 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
 Db 1516 GAGAAAGTGTCTCTATTTGCAGAAAGGAAAGCAGCTGCGGTATTTGTGAAATGCCATGAC 1575
 Qy 441 LysSerLeuAsnLysLysSerGly 448
 Db 1576 AAGTCTCTGAATAAGAGTCAGGC 1599
 RESULT 4
 US-10-755-889-99
 ; Sequence 99, Application US/10755889
 ; Publication No. US20040171823A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
 ; TITLE OF INVENTION: PATHWAY
 ; FILE REFERENCE: D0284 NP
 ; CURRENT APPLICATION NUMBER: US/10/755,889
 ; CURRENT FILING DATE: 2004-01-13
 ; ERROR APPLICATION NUMBER: U.S. 60/440,068
 ; PRIOR FILING DATE: 2003-01-14
 ; PRIOR APPLICATION NUMBER: U.S. 60/469,757
 ; PRIOR FILING DATE: 2003-05-12
 ; NUMBER OF SEQ ID NOS: 823
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 99
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-755-889-99
 Alignment Scores:
 Pred. No.: 5,18e-277 Length: 3549
 Score: 2385.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 17 Gaps: 0
 US-10-019-341-3 (1-448) x US-10-755-889-99 (1-3549)
 Qy 1 AlaAspGlnArgArgPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
 Db 256 GCCGACCAAGAAAGAGATTTTATCGACATCGAAAGTAATTTGCCCTTAGGACCCCTGAA 315
 Qy 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
 Db 316 GACACAGCTGAGGACACTTGCACCTCATTCCTCCGAGTAGCAGAGTCCGTGGCTACCTGT 375
 Qy 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTrpThrValThrGlyMet 60
 Db 376 CATTTCAATACACAGCAGCAAACTTCTGTGTGTATCATGCTGCGGTAAACAGGAATG 435
 Qy 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80
 Db 436 TATGAGAGTGGTGGCCAAACTTGTGGCCGCTGTACAAAGAGAGAACCCAGACTCCCAAT 495
 Qy 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
 Db 496 GTCATTGTGTGGTGTGCTGCTGCGGCTCAGGAGCAATACCCAGTGTCCGCGGCTAC 555
 Qy 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120
 Db 556 ACCAAACTGGTGGGACAGAGTGTGGCCGGTTTATCACTGGATGGAGGAGGTTTAAAC 615
 Qy 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaGlyTyr 140
 Db 616 TACCTCTGGACATGTCTCTTGGATACAGCTTGGAGCCCATGCTCTGGCATT 675

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QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
Db 676 GCAGGAAGTCTGACCAATAAGAAAGTCAACAGAAATTAATCTGGCCCTCGATCAGCTGGACCT 735
QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAlaAspPheValAsp 180
Db 736 AACTTTGAGTATGCAGAGCCCGAGTCTCTTCTCTGATGATGCAGATTTGTAGAC 795
QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
Db 796 GTCTTACACACATTACACAGAGGTCCTCTGGTGGAGCAATTTGGAATCCAGAAACAGATT 855
QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
Db 856 GGGCATGTGTACATTTACCGAATGGAGGTACTTTTCAGCCAGGATGTAACATTTGAGAA 915
QY 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
Db 916 GCTATCCCGGTGATTGCAGAGAGAGGACTTGGAGATGTGACCACTAGTGAAGTGTCTCC 975
QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
Db 976 CACGAGCGCTCCATTCATCTCTTCATCGACTCTCTGTTGAATGAAGAAATCCAAAGTAAG 1035
QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
Db 1036 GCCTACAGGTGCAGTTCACAGAGCGCTTTCAGAAAGGGCTCTGTTGAGTTGTAGAAG 1095
QY 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerLys 300
Db 1096 AACCGCTGCAACAATCTGGGTATGAGATCAATAAAGTCAGAGCCAAAGAGAGCAGCAA 1155
QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
Db 1156 ATGTACCTGAGACTGTCTTCAGATGCCCTACAAAGTCTTCCATTACCAAGTAAGATT 1215
QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
Db 1216 CATTTTCTGGGACTGAGAGTGAAACCCATACCAATCAGGCTTTCAGATTTCTCTGTAT 1275
QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
Db 1276 GGCACCTGGCCGAGAGTGAGAAATCCATCTCTGCTGAGTTCACCAATTAAG 1335
QY 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeu 380
Db 1336 ACCTACTCTCTCTTAATTTACAGAGGTAGATTTGGAGAACTACTCATGTTGAAGCTC 1395
QY 381 LysTyrLysSerAspSerTyrPheSerTyrPheSerTyrPheSerProGlyPheAla 400
Db 1396 AAATGGAAGAGTGTATTCATCTTATGCTGTGAGACTGGTGGAGCAGTCCCGGCTTCGCC 1455
QY 401 IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
Db 1456 ATTCAAGATTCAGATTAAGAGAGAGAGAGACTCAGAAAAAGGTATCTTCTGTCTTAGG 1515
QY 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
Db 1516 GAGAAAGTGTCTCATTTTGCAGAAAGAAAGGACCTCGCGGTATTTGTGAATGCCATGAC 1575
QY 441 LysSerLeuAsnLysLysSerGly 448
Db 1576 AAGTCTCTGAATAAGAAGTCAGGC 1599

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RESULT 5

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US-10-116-802-28
; Sequence 28, Application US/10116802
; Publication No. US20030065157A1
; GENERAL INFORMATION:
; APPLICANT: Amy Lasek
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US

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; CURRENT APPLICATION NUMBER: US/10/116,802
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,593
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 28
; LENGTH: 3635
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 3950154CB1
US-10-116-802-28

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Alignment Scores:

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Pred. No.: 3,78e-276 Length: 3635
Score: 2378.00 Matches: 447
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.78% Mismatches: 0
Query Match: 99.71% Indels: 0
DB: 14 Gaps: 0

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US-10-019-341-3 (1-448) x US-10-116-802-28 (1-3635)

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QY 1 AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
Db 331 GCCGACCACAAAGAGAGATTTTATCGACATCGAAAGTAATTTGCCCTAAGGACCCCTGAA 390
QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
Db 391 GACACAGCTGAGGACACTTGCACCTCATTCGCCGAGTAGCAGAGTCGCTGGCTACCTGT 450
QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTyrThrValThrGlyMet 60
Db 451 CATTTCAATCACACACACAAACCTTCATGTGTATCAATGGCTGGACGGTAACAGGAATG 510
QY 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80
Db 511 TATGAGAGTTGGGTGCCAAACCTTGTGCCGCCCTGTACAAGAGAGAACCCAGACTCCAAT 570
QY 81 ValIleValIleAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
Db 571 GTCAATGTGTGGACTGGCTGTACGGGCTCAGGAGCATTACCAGTGTCGGCGGCTAC 630
QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120
Db 631 ACCAACTGTGGGACAGGATGTGGCCGGTTTATCAACTGGATGGAGAGGAATTTAAC 690
QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyIle 140
Db 691 TACCTCTTGACAATGTCCATCTCTTGGGATACAGCCTTGGAGCCCATGCTGTCTGCATT 750
QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
Db 751 GCAGGAAGTCTGACCAATAAGAAAGTCAACAGAATTAATCTGGCTCGATCCAGCTGGACCT 810
QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
Db 811 AACTTTGAGTATGCAGAGCCCGAGTCTCTTCTCTGATGATGCAGATTTGTAGAC 870
QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
Db 871 GTCTTACACACATTACACAGAGGTCCTCTGGTGGAGGATTTGGAATCCAGAAACAGATT 930
QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
Db 931 GGGCATGTGTGACATTTACCCGGAATGAGGAGTACTTTTCAGCCAGGATGTAACATTTGAGAA 990
QY 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
Db 991 GCTATCCCGCTGATTTGCAGAGAGAGACTTTGGAGATGTGGACCTAGCTAGTAGTCTCC 1050

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| | | | |
|---|-----------|--|------|
| QY | 241 | HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluLeuAsnProSerLys | 260 |
| DB | 1051 | CACGAGCGCTCCATTCATCTCTTCATCGACTCTCTGTGAATGAAGAAAATCAAGTAAG | 1110 |
| QY | 261 | AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys | 280 |
| DB | 1111 | GCCTACAGGTGCAGCTTCCAAAGGAAGCCTTTGAGAAAGGGCTCTGCTTGAGTTGTAGAAG | 1170 |
| QY | 281 | AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerLys | 300 |
| DB | 1171 | AACCGCTGCACCAATCTGGGCTATGAGATCAATAAAGTCAGAGCCAAAGAGCAGCAA | 1230 |
| QY | 301 | MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle | 320 |
| DB | 1231 | ATGTACCTGAAGACTCGTTCTCAGATGCCCTACAAAGTCCTCCATTACCAAGTAAGATT | 1290 |
| QY | 321 | HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr | 340 |
| DB | 1291 | CATTTTCTGGGACTGAGAGTGAACCCATCAATCAAGCTTTCAGATTTCTCTGTAT | 1350 |
| QY | 341 | GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys | 360 |
| DB | 1351 | GGCACCGTGGCGGAGAGTGAGACATCCCATTCATCTGCTGAGTTTCCACAAATAAG | 1410 |
| QY | 361 | ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeu | 380 |
| DB | 1411 | ACCTACTCTCTCTAAATTTACACAGAGGTAGATATTGAGAACTACTCATGTGTGAAGCTC | 1470 |
| QY | 381 | LysTyrLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerSerProGlyPheAla | 400 |
| DB | 1471 | AAATGGAAGAGTGATTCATCTATTTAGCTGGTCAGACTGGTGAGCAGCTCAGAAAAGTGATCTTCTGTTCTAGG | 1530 |
| QY | 401 | IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg | 420 |
| DB | 1531 | ATTCAAGATCAGAGTAAACAGCAGAGAGACTCAGAAAAGTGATCTTCTGTTCTAGG | 1590 |
| QY | 421 | GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp | 440 |
| DB | 1591 | GAGAAAGTGCTCTCATTTGCAAGAAAGAAAGGACCTGCGGTATTTGTGAATGCCATGAC | 1650 |
| QY | 441 | LysSerLeuAsnLysLysSerGly | 448 |
| DB | 1651 | AAGTCTCTGAATAAGAAAGTCAGGC | 1674 |
| RESULT 6 | | | |
| US-09-971-392-107 | | | |
| ; Sequence 107, Application US/09971392 | | | |
| ; Publication No. US20030134283A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Peterson, David P. | | | |
| ; APPLICANT: Peterson, Cecelia I. | | | |
| ; APPLICANT: Cocks, Benjamin G. | | | |
| ; TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CELL DIFFERENTIATION | | | |
| ; FILE REFERENCE: PA-0029 US | | | |
| ; CURRENT APPLICATION NUMBER: US/09/971,392 | | | |
| ; CURRENT FILING DATE: 2001-10-03 | | | |
| ; PRIOR APPLICATION NUMBER: 60/237,652 | | | |
| ; PRIOR FILING DATE: 2000-10-03 | | | |
| ; NUMBER OF SEQ ID NOS: 260 | | | |
| ; SOFTWARE: PERL Program | | | |
| ; SEQ ID NO 107 | | | |
| ; LENGTH: 4075 | | | |
| ; TYPE: DNA | | | |
| ; ORGANISM: Homo sapiens | | | |
| ; FEATURE: | | | |
| ; NAME/KEY: misc feature | | | |
| ; OTHER INFORMATION: Template ID: 049457.6 | | | |
| US-09-971-392-107 | | | |
| Alignment Scores: | | | |
| Pred. No.: | 2,41e-275 | Length: | 4075 |
| Score: | 2372.00 | Matches: | 448 |
| Percent Similarity: | 99.78% | Conservative: | 0 |

| | | | |
|--|--------|--|------|
| Best Local Similarity: | 99.78% | Mismatches: | 0 |
| Query Match: | 99.45% | Indels: | 1 |
| DB: | 10 | Gaps: | 0 |
| US-10-019-341-3 (1-448) x US-09-971-392-107 (1-4075) | | | |
| QY | 1 | AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu | 20 |
| DB | 750 | GCCGACCAAGAGAGATTTTATCGACATCGAAGTAAATTTGCCCTTAAGGACCCCTGAA | 809 |
| QY | 21 | AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys | 40 |
| DB | 810 | GACACAGCTGAGGACACTTCCACCTCATTTCCCGAGTAGCAGAGTCGCTGGCTACCTGT | 869 |
| QY | 41 | HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTyrThrValThrGlyMet | 60 |
| DB | 870 | CATTTCAATCACACAGCAAAACCTTTCATGGTGATTCATGGCTGCGGTAAACAGGAATG | 929 |
| QY | 61 | TyrGluSerTrpValProLysLeuValAlaLeuTyrLysArgGluProAspSerAsn | 80 |
| DB | 930 | TATGAGAGTTGGTGCCAAACTTGTGSCCGCCTGTACAAGAGAGAACCCAGACTCCAAAT | 989 |
| QY | 81 | ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr | 100 |
| DB | 990 | GTCAATTGTGTGGACTGGCTGTCCGGCTCAGGAGCAATACCCAGTGTCCGCGGCTAC | 1049 |
| QY | 101 | ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn | 120 |
| DB | 1050 | ACCAAACTGGTGGGACAGAGATGTGCGCGGTATTAACCTGATGGAGGAGAGTTTAAAC | 1109 |
| QY | 121 | TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyIle | 140 |
| DB | 1110 | TACCTCTGGCAATGTCCATCTCTTGGGATACAGCCTTGGAGCCCATGTCTGTGGCATT | 1169 |
| QY | 141 | AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro | 160 |
| DB | 1170 | GCAGGAAGTCTGACCAATAAGAAAGTCAACAGAAATTACTTGGCCTCGATCCAGCTGGACCT | 1229 |
| QY | 161 | AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp | 180 |
| DB | 1230 | AACTTTGAGTATGCAAGAGCCCGAGTCTCTTTCTCTGATGATGCAGATTTGTAGAC | 1289 |
| QY | 181 | ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal | 200 |
| DB | 1290 | GTCTTACACACATTCACAGAGGGTCCCTGCTGCGAAGCATTTGGAATCCAGAAACCCAGTT | 1349 |
| QY | 201 | GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu | 220 |
| DB | 1350 | GGGCATGTTGACATTTACCCGAATGGAGGTACTTTTCAGCCAGGATGTAAACATTGGAGAA | 1409 |
| QY | 221 | AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer | 240 |
| DB | 1410 | GCATATCCGCGTGAATTCACAGAGAGACTTGGAGATGTGACAGCTAGTGAAGTGTCTCC | 1469 |
| QY | 241 | HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGlnProSerLys | 260 |
| DB | 1470 | CACGAGCGCTCCATTCATCTCTCATCGACTCTCTGTGAATGAAGAAATCCAAAGTAAG | 1529 |
| QY | 261 | AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys | 280 |
| DB | 1530 | GCCTACAGGTGCGATTTCCAAAGGAGCCTTTGAGAAAGGGCTCTGCTTGTAGTGTAGAAAG | 1589 |
| QY | 281 | AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys | 300 |
| DB | 1590 | AACCGTGCACCAATCTGGGCTATGAGATCAATAAAGTCAGAGCCAAAGAGCAGCAAA | 1649 |
| QY | 301 | MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle | 320 |
| DB | 1650 | ATGTACCTGAAGACTCGTTCTCAGATGCCCTACAAAGCTTTCATTAACCAAGTAAGATT | 1709 |
| QY | 321 | HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr | 340 |
| DB | 1710 | CATTTTCTGGGACTGAGAGTGAAACCCATACCAATCAGGCCCTTTGAGATTTCTCTGTAT | 1769 |

QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
Db 1770 GGCACCGTGGCCGAGAGTGGAGACATCCCATCTCCCTGAAGTTTCCCAATAAAG 1829
QY 361 ThrTyrSerPheLeuIleTyrGluValAspIleGlyGluLeuMetLeuLysLeu 380
Db 1830 ACCTACTCTCTCTAATTTACACAGAGGTAGATATTGGAGAACTACTCATGTTGAAGCTC 1889
QY 381 LysTrpLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerSerProGlyPheAla 400
Db 1890 AAATGGAAGAGTATCTACTTTTACAGAGGTAGATATTGGAGAACTACTCATGTTGAAGCTC 1949
QY 401 Ile-GlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerAr 420
Db 1950 ATTGAGAGATCAGNGTAAAGCAGAGAGACTCAGAAAAGGTGATCTTCTGTCTAG 2009
QY 420 gGluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAs 440
Db 2010 GGAGAAAGTGTCTCATTTGCAGAAAGGAAAGGCACCTCGGCTATTGTGAATGCAATGA 2069
QY 440 pLysSerLeuAsnLysLysSerGly 448
Db 2070 CAAGTCTCTGAATAAGAGTCAGGC 2094

RESULT 7

US-10-388-934-188
; Sequence 188, Application US/10388934
; Publication No. US2004000547A1
; GENERAL INFORMATION:
; APPLICANT: Boess, Franziska
; APPLICANT: Suter-Dick, Laura
; APPLICANT: Wolf, Detlef
; TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
; FILE REFERENCE: 21199
; CURRENT APPLICATION NUMBER: US/10/388,934
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 02005336.9
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 02015657.6
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 862
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 188
; LENGTH: 3617
; TYPE: DNA
; ORGANISM: Rattus norvegicus (No. US20040005547Alway rat)
US-10-388-934-188

Alignment Scores:

Pred. No.: 6.41e-259 Length: 3617
Score: 2235.50 Matches: 416
Percent Similarity: 96.65% Conservative: 17
Best Local Similarity: 92.86% Mismatches: 14
Query Match: 93.73% Indels: 1
DB: Gaps: 1

US-10-019-341-3 (1-448) x US-10-388-934-188 (1-3617)

QY 1 AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
Db 256 GCAGACGGGGGAAGAGATTCTCAGACATCGAAAGTAAATTTGCCCTAAGGACCCCTGAA 315
QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
Db 316 GACACAGCTGAGACACTGTCTATCTGATTCCTGGATTAGCAGACTCTGTGTCTAACTGC 375
QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTrpThrValThrGlyMet 60
Db 376 CACTTCACACAGCAGCAAAACCTTTGTGGTATCCATCGATCGAGCGGTGACAGGAATG 435
QY 61 TyrGluSerTrpValProLysLeuValAlaLeuTyrLysArgGluProAspSerAsn 80

Db 436 TATGAGAGTTGGTGGCCCAAACTTGTGGCTGCCCTATACAAAAGAGAACCTGACTCCAAT 495
QY 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
Db 496 GTCAITGTAGTAGACTGGTTGTATCGGGCCGACACATATTCAGTGTCTCGCGGTAT 555
QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluPheAsn 120
Db 556 ACCAAGCTGTGGAAATGATGTGCCAGGTTTCATCACTGCTGGAGGAGAAATTTAAC 615
QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaGlyIle 140
Db 616 TACCCCTTAGACAATGTCCACTCTTAGGGTACAGTCTTTGGAGCCCATCTGCTGGCGTG 675
QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
Db 676 GCAGAGAGTCTGACCACACAGNAGGTCAATAGAAATTTACTGGCTTGGATCCAGCTGGGCT 735
QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
Db 736 AACTTTGAGTATGCAGAAAGCCCTAGTCGCTTTCTCTGATGATGCGGATTTCTGATAT 795
QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
Db 796 GTCTTACACACATTTACCAGGGGGTGGCTGTGTCGAGTATTGGATCCAGAAACAGTA 855
QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
Db 856 GGGCATGTTGATATTTATCCCAATGGAGGCATTTCCAGCCAGGATGCAACATTTGGAGAA 915
QY 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
Db 916 GCCATTGCTGTAATGTCAGAGAGGGCTTGGAGATGTGGACCACTGCTGAAGTGTCTCG 975
QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
Db 976 CACGAGCGCTCCATCCATCTCTTATTGACTCCCTGCTGTAATGAAGAAACCCAGCAAG 1035
QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
Db 1036 GCATACAGGTGCATTTCCAGGAGGCTTTGAGAAAGGGCTCTGCTGAGTTGCAGAAAG 1095
QY 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys 300
Db 1096 AATCGCTGTAACAACGTGGGCTATGAGATCAACAAGGTTCAGAGCCAGAGAGCAGTAAG 1155
QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
Db 1156 ATGTACCTGAAGACTCGCTCTCAGATGCCCTTACAAAGTATTTCATTACCAAGTCAAGATT 1215
QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
Db 1216 CACTTTTCTGGAAGTGCATGATGACAGCAACCAACAGGCTTCGAGATTTCTCTGAT 1275
QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
Db 1276 GGCACAGTGGCTGAAAGTGAGAACATTTCCCTTCAACCTGCGGAGGTTCGCCACAAATAA 1335
QY 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGlnLeuLeuMetLeuLysLeu 380
Db 1336 ACCTACTCTCTTGTGATTTACCGAGGTGAGATCGGGGAATTTGCTGATGATGAAGCTT 1395
QY 381 LysTrpLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerSerProGlyPheAla 400
Db 1396 AAGTGGAGAGACACTCTTACTTCCGCTGTGAGCTGTGGAGAGCTCCAGCTTTGTC 1455
QY 401 IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
Db 1456 ATCGAAGATCCGAGTGAAGCCGAGAGACTCAGAAAAGGTCTATCTTCTGTGCCAGG 1515
QY 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
Db 1516 GAGAAAGTTTCTCATCTGCAGAAAGGAGGAGCGCTGCAGTGTTCGTGAATGCCATGAC 1575

QY 400 AlaileGlnLysIleArgValLysAlaGluThrGlnLysLysValIlePheCysSer 419
 Db 1584 AATATCAGCGCATCGGGTGAAGTCTGGGAAACCCAGCGGAACATGACATTTGTACA 1643
 QY 420 ArgGluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHis 439
 Db 1644 GAAGACCTTGAGAACACACCATATCCCGCGGAGCTCTGGTTTCGCAAGTGTGCG 1703
 QY 440 Asp 440
 Db 1704 GAT 1706

RESULT 9

US-10-354-358-45
 ; Sequence 45, Application US/10354358
 ; Publication No. US20030157082A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc
 ; APPLICANT: Hunter, John Joseph
 ; APPLICANT: Macbeth, Kyle J.
 ; APPLICANT: Tsai, Fong-Ying
 ; APPLICANT: Lesoon, Andrea
 ; APPLICANT: Lightcap, Eric S.
 ; APPLICANT: Williamson, Mark
 ; APPLICANT: Rudolph-Owen, Laura A.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
 ; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
 ; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
 ; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
 ; TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
 ; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
 ; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
 ; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
 ; FILE REFERENCE: MP102-020P1RNM0NM1M
 ; CURRENT APPLICATION NUMBER: US/10/354,358
 ; CURRENT FILING DATE: 2003-01-30
 ; PRIOR APPLICATION NUMBER: US 60/353,600
 ; PRIOR FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: US 60/364,517
 ; PRIOR FILING DATE: 2002-03-15
 ; PRIOR APPLICATION NUMBER: US 60/371,075
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: US 60/371,507
 ; PRIOR FILING DATE: 2002-04-10
 ; PRIOR APPLICATION NUMBER: US 60/372,984
 ; PRIOR FILING DATE: 2002-04-16
 ; PRIOR APPLICATION NUMBER: US 60/374,194
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: US 60/382,995
 ; PRIOR FILING DATE: 2002-05-24
 ; PRIOR APPLICATION NUMBER: US 60/385,023
 ; PRIOR FILING DATE: 2002-05-31
 ; PRIOR APPLICATION NUMBER: US 60/388,853
 ; PRIOR FILING DATE: 2002-06-14
 ; PRIOR APPLICATION NUMBER: US 60/389,395
 ; PRIOR FILING DATE: 2002-06-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: Fast-Seq for Windows Version 4.0
 ; SEQ ID NO 45
 ; LENGTH: 3927
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (253)....(1755)
 US-10-354-358-45

Alignment Scores:

Pred. No.: 6,42e-129 Length: 3927
 Score: 1161.00 Matches: 216
 Percent Similarity: 69.16% Conservative: 89
 Best Local Similarity: 48.98% Mismatches: 118

Query Match: 48.68% Indels: 18
 DB: 15 Gaps: 6
 US-10-019-341-3 (1-448) x US-10-354-358-45 (1-3927)
 QY 13 LysPheAlaLeuArgThrProGluAspThrAlaGluAspThrCysHisLeuIleProGly 32
 Db 400 AGGTTTAACTTCGCGACCTCCAGAGCCAGAGCATGAAGATGCTACCTCTCGTCGCG 459
 QY 33 ValAlaGluSerValAlaThrCysHisPheAsnHisSerSerLysThrPheMetValIle 52
 Db 460 CACAGCCAGCCCTTAGAAGACTGAGTTTCAACATGACAGCTAAACCTTTTTCATCAT 519
 QY 53 HisGlyTrpThrValThrGlyMetTyrGluSerTrpValProLysLeuValAlaLeu 72
 Db 520 CACGGATGACGATGAGCGGTATCTTTGAAACTGGCTGCACAACTCTGTGTCAGCCCTG 579
 QY 73 TyrLysArgGluProAspSerAsnValIleValValAspTrpLeuSerArgAlaGlnGlu 92
 Db 580 CACACAAGAGAGAAAGACGCCAATGATGTGTGTGTTGACTGGCTCCCTCGGCCACAC 639
 QY 93 HisTyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAlaArgPheIle 112
 Db 640 CTTTACCGATGCGGTCAATAATACCGGGTGGGACACAGCATTCGCCAGGATGCTC 699
 QY 113 AsnTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSer 132
 Db 700 GACTGCTGCAGAGAGACGAGATTTTCTCTCGGAATGTCCTTGTATCGGTACAGC 759
 QY 133 LeuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysLysValAsnArgIle 152
 Db 760 CTCGAGCGCACGTGGCGGGTATGACGAGCAACTTCGTGAAAGGAACGCTGGCGCGAATC 819
 QY 153 ThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSer 172
 Db 820 ACAGGTTTGGATCTGCGGGCCCATGTTTGAAGGGCCGACATCCACAAGAGGCTCTCT 879
 QY 173 ProAspAlaAspPheValAspValLeuHisThrPheThrArgGlySerProGlyArg 192
 Db 880 CCGGACGATGAGATTTTGTGATGCTCTCCACACCTACACGCGT--TCCTTCGGCTTG 936
 QY 193 SerIleGlyIleGlnLysProValGlyHisValAspIleTyrProAsnGlyThrPhe 212
 Db 937 AGCATTTGTAATTCAGATGCTGTGGCCACATTCACATCTACCCCAATGGGGTGACTTC 996
 QY 213 GlnProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAsp 232
 Db 997 CAGCCAGCTGTGACTCAGCATGCTTGGGATCAATTGCA-----TATGGGAACA 1047
 QY 233 ValAspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeu 252
 Db 1048 ATCAGAGGTGTGTAATAATGTGAGCATGAGGAGCCCTCCACCTCTTTGTGTGATCTCTG 1107
 QY 253 LeuAsnGluGluAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLys 272
 Db 1108 GTGAATCAGACAAGCCGAGTTTTCCTCCAGTGCACTGACTCAATCGCTTCAAAAAG 1167
 QY 273 GlyLeuCysLeuSerCysArgLysAsnArgCysAsnAsnLeuGlyTyrGluIleAsnLys 292
 Db 1168 GGGATCTGTGAGCTGCCCAAGAACCCGTGTGAATAGCATTTGGTACAAATGCCAAGAA 1227
 QY 293 ValArgAlaLysArgSerSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLys 312
 Db 1228 ATGAGGAACAAGAGGAACAGCAAAATGTACTTAAACCCCGGACGAGCATGCTTTTCAGA 1287
 QY 313 ValPheHisTyrGlnValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsn 332
 Db 1288 GTTACCATTTATCAGATGAATAATCCATGCTTCAGTTACAGAATCATGGTACAAATGCCAAGAA 1347
 QY 333 GlnAlaPheGluIleSerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThr 352
 Db 1348 CCCACCTTTTACGTACCCCTTTATGGCACTAATGTCAGATTCACAGACTCTGCCACTGGAA 1407

| Alignment Scores: | | | | | |
|---|-----------|--|------------|--|--|
| Pred. No.: | 6.42e-129 | Length: | 3927 | | |
| Score: | 1161.00 | Matches: | 216 | | |
| Percent Similarity: | 69.16% | Conservative: | 89 | | |
| Best Local Similarity: | 48.98% | Mismatches: | 118 | | |
| Query Match: | 48.68% | Indels: | 18 | | |
| DB: | 15 | Gaps: | 6 | | |
| US-10-019-341-3 (1-448) x US-10-172-118-1234 (1-3927) | | | | | |
| Qy | 13 | LyspheAlaLeuArgThrProGluAspThrAlaGluAspThrCysHisLeuIleProGly | 32 | | |
| | | ::::: | ::::: | | |
| Dd | 400 | AGGTTTAACCTCCGCACCCTCCAGAGCCACGAGCATGAAGATGCTTACCTTCGGTCGGC | 459 | | |
| | | ::::: | ::::: | | |
| Qy | 33 | VallAlaGluSerValAlaThrCysHisPheAsnHisSerSerylsthRheMetValIle | 52 | | |
| | | ::::: :::: | ::::: :::: | | |
| Dd | 460 | CACAGCCGCCGCTTAGAAGACTGCAGTTTCACATGACGAGCTAAACCTTTTCATCAATT | 519 | | |
| | | ::::: :::: | ::::: :::: | | |
| Qy | 53 | HisGlyTrpThrValThrGlyMetTyrGluSerTrpValProLysLeuValAlaAlaLeu | 72 | | |
| | | ::::: :::: | ::::: :::: | | |

QY 420 ArgGluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHis 439
 Db 1645 GAAGACCTCTGAGAACACACCATATCCCGAGCGGGAGCTCTGGTTTCGCAAGTCTCGG 1704
 QY 440 Asp 440
 Db 1705 GAT 1707

RESULT 11

US-10-211-462-228
 ; Sequence 228, Application US/10211462
 ; Publication No. US20040033495A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Murray, Richard
 ; APPLICANT: Glynn, Richard
 ; APPLICANT: Watson, Susan R.
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Eos Biotechnology, Inc.
 ; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
 ; FILE REFERENCE: 018501-006200US
 ; CURRENT APPLICATION NUMBER: US/10/211,462
 ; PRIOR FILING DATE: 2003-02-13
 ; PRIOR APPLICATION NUMBER: US 09/784,356
 ; PRIOR FILING DATE: 2001-02-14
 ; PRIOR APPLICATION NUMBER: US 09/791,390
 ; PRIOR FILING DATE: 2001-02-22
 ; PRIOR APPLICATION NUMBER: US 60/310,025
 ; PRIOR FILING DATE: 2001-08-03
 ; PRIOR APPLICATION NUMBER: US 60/334,244
 ; PRIOR FILING DATE: 2001-11-29
 ; NUMBER OF SEQ ID NOS: 230
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 228
 ; LENGTH: 3927
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-211-462-228

Alignment Scores:

Pred. No.: 6.42e-129 Length: 3927
 Score: 1161.00 Matches: 216
 Percent Similarity: 69.16% Conservative: 89
 Best Local Similarity: 48.98% Mismatches: 118
 Query Match: 48.68% Indels: 18
 Gaps: 6

US-10-019-341-3 (1-448) x US-10-211-462-228 (1-3927)

QY 13 LysPheAlaLeuArgThrProGluAspThrAlaGluAspThrCysHisLeuIleProGly 32
 Db 400 AGGTTAACTCCGACCTCCAGAGCCGAGCATGAAGATGCTCTCTCGTCGGC 459
 QY 33 ValAlaGluSerValAlaThrCysHisPheAsnHisSerSerLysThrPheMetValIle 52
 Db 460 CACAGCCAGCCCTTAGAGACTGCGAGTTCCACATGACAGCTAAACCTTTTCATCATT 519
 QY 53 HisGlyTrpThrValThrGlyMetTyrGluSerTrpValProLysLeuValAlaAlaLeu 72
 Db 520 CACGGATGACATGACGCGGTATCTTTGAAACCTGGCTGCACAACTCGTGTGAGCCCTG 579
 QY 73 TyrLysArgGluProAspSerAsnValIleValValAspThrLeuSerArgAlaGlnGlu 92
 Db 580 CACACAGAGAGAAGACGCCAATGTAGTTGTGCTTCACTGGCTCCCTCCGCCCCACAG 639
 QY 93 HisTyrProValSerAlaGlyTyrThrLysLeuValGlnAspValAlaAlaArgPheIle 112
 Db 640 CTTTACAGGATCGGTCAATAATACAGGGTGTGGGACACAGCATTCGACGATGCTC 699
 QY 113 AsnTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSer 132
 Db 700 GACTGGTGCAGGAGAGGACGATTTTCTCTCGGGAATGTCCACTTGATCGCTACAGC 759

QY 133 LeuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysLysValAsnArgIle 152
 Db 760 CTCGAGCGCACGTGCGCGGTATGAGGCAACTCTGTGAAAGAACGCTGGGCCGGAATC 819
 QY 153 ThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSer 172
 Db 820 ACAGGTTTGGATCTCTGCGGGGCCCATGTTTGAAGGGCGGCACATCCACAGAGGCTCTCT 879
 QY 173 ProAspAlaAspPheValAspValLeuHisThrPheThrArgGlySerProGlyArg 192
 Db 880 CCGGACGATGCAGATTTTGTGATGTCCTCCACACCTACACGGT---TCTTCGGCTTG 936
 QY 193 SerIleGlyIleGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPhe 212
 Db 937 AGCATTTGTTTATTCAGATGCTGTGGCCACATTTGACATCTACCCNANTGGGGTGACTTC 996
 QY 213 GlnProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAsp 232
 Db 997 CAGCCAGGCTGTGGACTCAACGATGCTTTGGGATCAATTGCA-----TATGGAACA 1047
 QY 233 ValAspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeu 252
 Db 1048 ATCAGAGGTGCTTAATGTGAGCATGAGCGCGCTCCACCTCTTTGTTGACTCTCTG 1107
 QY 253 LeuAsnGluGluAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLys 272
 Db 1108 GTGAATCAGGACAGCCGAGTTTTCCTTCAGTGCATGCTCCAAATCGCTTCAAAAG 1167
 QY 273 GlyLeuCysLeuSerCysArgLysAsnArgCysAsnAsnLeuGlyTyrGluIleAsnLys 292
 Db 1168 GGGATCTCTGAGTGCAGCGCAAGACCGTTGTAATAGCATTTGGCTCAACTGCCAAGAAA 1227
 QY 293 ValArgAlaLysArgSerSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLys 312
 Db 1228 ATGAGGAACAAGAGACAGCAAAATGTACCTAAACCCCGGAGGAGGATGCTTTTCAGA 1287
 QY 313 ValPheHisTyrGlnValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsn 332
 Db 1288 GTTTACCATTTATCAGATGAAATCCATGCTCTTCAGTTACAGACATCGGAGAAATTGAG 1347
 QY 333 GlnAlaPheGluIleSerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThr 352
 Db 1348 CCCACCTTTTACGTCACTCTTATGGCACTAATGCAGATTCCAGACTCTCCACTCGAA 1407
 QY 353 LeuProGlu---ValSerThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAsp 371
 Db 1408 ATAGTGGAGCGGATCGAGAGAAATGCCCAACACCTTCTCTGGTCTACACGAGGAGGAC 1467
 QY 372 IleGlyGluLeuLeuMetLeuLysLeuLysTrpLysSerAspSerTyrPheSerTrpSer 391
 Db 1468 TTGGAGACCTCTTTGAAGATCCAGCTCACCTGGAGGGGGCTCTAG---TCTTGTGATC 1524
 QY 392 AspTrpTrpSer-----SerProGly-----Phe 399
 Db 1525 AACCTGTGAGGAGGAGTTTCGAGCTACTGCTCTCAACCCCGCAACCCCGAGCGGAGCTG 1584
 QY 400 AlaIleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSer 419
 Db 1585 AATATCAGGCGCATCCCGGTGAAGTCTGGGGAACCCAGCGGAACTGACATTTTGTACA 1644
 QY 420 ArgGluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHis 439
 Db 1645 GAAGACCTCGAGAACACACCATATCCCGAGCGGGAGCTCTGGTTTTCGCAAGTCTCGG 1704
 QY 440 Asp 440
 Db 1705 GAT 1707

RESULT 12

US-10-342-887-1234
 ; Sequence 1234, Application US/10342887
 ; Publication No. US20040058340A1

; LOCATION: (253) ... (1755)
US-10-319-915-4

Alignment Scores:

Pred. No.: 6,42e-129 Length: 3927
Score: 1161.00 Matches: 216
Percent Similarity: 69.16% Conservatives: 89
Best Local Similarity: 48.98% Mismatches: 118
Query Match: 48.68% Indels: 18
DB: 17 Gaps: 6

US-10-019-341-3 (1-448) x US-10-319-915-4 (1-3927)

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QY 13 LysPheAlaLeuArgThrProGluAspThrAlaGluAspThrCysHisLeuLeuProGly 32
Db 400 AGGTTTAACTCCGACCTCCAGGACCCAGAGCATGAAGGATGTACCTCTCCGTCGGC 459

QY 33 ValAlaGluSerValAlaThrCysHisPheAsnHisSerSerLysThrPheMetValile 52
Db 460 CACAGCCAGCCCTTGAAGACTGCAGTTTCAACATGACAGCTAAACCTTTTCATCAT 519

QY 53 HisGlyTrpThrValThrGlyMetTyrGluSerTrpValProLysLeuValAlaLeu 72
Db 520 CACGATGACATGAGCGGTATCTTGAATACTGGCTGCACAAACTCGTGTACGCCCTG 579

QY 73 TyrLysArgGluProAspSerAsnValileValValAspTrpLeuSerArgAlaGlnGlu 92
Db 580 CACACAGAGAGAGAGCCCAATGTAGTTGGTTGATCTGCCCTCCCTCCGCCACCCAG 639

QY 93 HisTyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAlaArgPheile 112
Db 640 CTTTACAGGATCGGTCAATAATACAGGGGTGGGACACAGCATTCGCCAGGATGCTC 699

QY 113 AsnTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuGlyTyrSer 132
Db 700 GACTGGCTGCGAGGAGAGGAGATTTTCTCTCGGGAATGTCCACTTCATCGGCTACAGC 759

QY 133 LeuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysLysValAsnArgile 152
Db 760 CTCGAGCGCACGTCGCGGGGTATGCAGCAACTTCGTGAAGAACCGTGGCGCAATC 819

QY 153 ThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSer 172
Db 820 ACAGTTTGGATCTCGCGGCCCATGTTTGAAGGGCGGACATCCACAGAGGCTCTCT 879

QY 173 ProAspAlaAspPheValAspValLeuHisThrPheThrArgGlySerProGlyArg 192
Db 880 CCGACCATGACAGATTTGTGGATGTCCTCCACACCTACACGCGT---TCCTCGGCTG 936

QY 193 SerIleGlyIleGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPhe 212
Db 937 AGCATTGTTATTCAGATGCTGTGGGACACATTCACATCTACCCCAATGGGGGTGACTTC 996

QY 213 GlnProGlyCysAsnIleGlyGluAlaIleArgValileAlaGluArgGlyLeuGlyAsp 232
Db 997 CAGCCAGGCTGTGACTCAACGATGTCTGGATCAATTGCA-----TATGGACA 1047

QY 233 ValAspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeu 252
Db 1048 ATCAGAGGGTGGTAAATATGACATGAGCAGCGCGTCCACCTCTTTTGTGACTCTCTG 1107

QY 253 LeuAsnGluGluAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLys 272
Db 1108 GTGAATCAGGACAGCCGAGTTTGGCTTCAGTGCACACTGACTCCAAATCGCTTCAAAAG 1167

QY 273 GlyLeuCysLeuSerCysArgLysAsnArgCysAsnAsnLeuGlyTyrGluIleAsnLys 292
Db 1168 GGGATCTGTCTGAGCTGCCGCAAGACCGTTGTAATAGCATTGCTGCTACATGCCAAGAA 1227

QY 293 ValArgAlaLysArgSerSerLysMetTyrIleuLysThrArgSerGlnMetProTyrLys 312
Db 1228 ATGAGGAACAGAGGAAACAGAAAATGTACTTAAACCCCGGCGAGCATGCTTTCAGA 1287

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QY 313 ValPheHisTyrGlnValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsn 332
Db 1288 GTTTACCATTCAGATGAATAATCCATGCTTCAGTTACAAGAACATGGGAGAAATTGAG 1347

QY 333 GlnAlaPheGluIleSerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThr 352
Db 1348 CCCACCTTTTACGTCACTCCCTTTATGCACTAATATGACAGATTCACCACTCTGCCACTGGAA 1407

QY 353 LeuProGlu---ValSerThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAsp 371
Db 1408 ATAGTGGAGCGGATCGAGCAGATGCCACCAACCTTCTGTCTACACCGAGGAGGAC 1467

QY 372 IleGlyGluLeuMetLeuLysLysLeuTyrLysSerAspSerTyrPheSerTrpSer 391
Db 1468 TTGGGAGACCTCTGAAGATCCAGCTCACCTGGAGGGGGCTCTCAG---TCTTGGTAC 1524

QY 392 AspTrpTrpSer-----SerProGly-----Phe 399
Db 1525 AACCTGTGGAAGAGATTTCGACGTACCTGTCTCAACCCCGCAACCCCGGAGGAGCTG 1584

QY 400 AlaIleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValilePheCysSer 419
Db 1585 AATATCAGCGCATCCGGTGAAGTCTGGGGAACCCAGCGGAACTGACATTTGTGATCA 1644

QY 420 ArgGluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHis 439
Db 1645 GAAGACCTCGAAGAACACACGAGCATATCCCGAGCGGGAGCTCTGTTTCGCAAGTCTCG 1704

QY 440 Asp 440
Db 1705 GAT 1707

RESULT 14
US-10-133-013-213
; Sequence 213, Application US/10133013
; Publication No. US20030166903A1
; GENERAL INFORMATION:
; APPLICANT: Astromoff, Anna
; APPLICANT: Bandman, Olga
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
; FILE REFERENCE: PA-0049 US
; CURRENT APPLICATION NUMBER: US/10/133,013
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/287,067
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PERL Program
; SEQ ID NO 213
; LENGTH: 4315
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030166903A1 400203.1
US-10-133-013-213

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Alignment Scores:
Pred. No.: 7,46e-129 Length: 4315
Score: 1161.00 Matches: 216
Percent Similarity: 69.16% Conservatives: 89
Best Local Similarity: 48.98% Mismatches: 118
Query Match: 48.68% Indels: 18
DB: 15 Gaps: 6

US-10-019-341-3 (1-448) x US-10-133-013-213 (1-4315)

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QY 33 ValAlaGluSerValAlaThrCysHisPheAsnHisSerLysThrPheMetValile 52
Db 565 AGGTTTAACTCCGACCTCCAGGACCCAGAGCATGAAGATGTACCTCTCGTCGGC 624

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625 CACAGCAGCCCTTAGAAGACTGCGATTTCAACATGACAGCTAAACCTTTTTCATCAT 684
53 HisGlyTrpThrValThrGlyMetTyrGluSerTrpValProLysLeuValAlaLeu 72
685 CACGATGACGATGAGCGGTATCTTTGAAACTGGCTGCACAACTCGTGTACGCCCTG 744
73 TyrLysArgGluProAspSerAsnValleValValAspTrpLeuSerArgAlaGlnGlu 92
745 CACACAGAGAGAAAGACGCAATGTAGTTGTGGTTGACTGGCTCCCTCGGCCACACAG 804
93 HisTyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAlaArgPheIle 112
805 CTTTACACGATGCGGTCAATTAATCCAGGGTGGTGGACACAGCATTCAGGATGCTC 864
113 AsnTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSer 132
865 GACTGCTGCAGGAGAGGACGATTTTCTCTCGGGAATGCTCACTGATCGGCTACAGC 924
133 LeuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysLysValAsnArgIle 152
925 CTCGAGCGGCACGTGGCGGGTATGACGACACTTCGTCAAGAGAACCGTGGGCCGATC 984
153 ThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSer 172
985 ACAGTTTGGATTCCTGCGGGCCCATGTTTGAAGGGCGGACATCCACAGAGGCTCTCT 1044
173 ProAspAlaAspPheValAspValLeuHisThrPheThrArgGlySerProGlyArg 192
1045 CCGGACGATGACATTTTGTGATGCTCTCCACACTACACGCGT---TCTTTCGGCTTG 1101
193 SerIleGlyIleGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPhe 212
1102 AGCATTTGGTATTTCAGATGCTGTGGCCACATGTGACATCTACCCCAATGGGGTGACTTC 1161
213 GlnProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAsp 232
1162 CAGCAGGCTGTGGACTCAACGATGCTTGGGATCAATTGCA-----TATGGAACA 1212
233 ValAspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeu 252
1213 ATCAGAGGTTGTTAAATGTGACATGACGAGCGGTCACCTCTTTTGTGACTCTCTG 1272
253 LeuAsnGluGluAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLys 272
1273 GTGAATCAGCAAGACGCGAGTTTGGCTTCCAGTGACACTGCCAATCGCTTCAAAAG 1332
273 GlyLeuCysLeuSerCysArgLysAsnArgCysAsnAsnLeuGlyTyrGluIleAsnLys 292
1333 GGGATCTGTGAGCTGCCGCAAGAACCGTTGTAATAGCATGGCTACAAATGCCAAGAA 1392
293 ValArgAlaLysArgSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLys 312
1393 ATGAGGAACAAGAGGAAACAGCAAAATGTACTTAAACACCGGCGGACATGCCCTTCAGA 1452
313 ValPheHisTyrGlnValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsn 332
1453 GTTTACCATTTATCAGATGAAATCCCATGCTTCAGTTACAAACATCGGAGAAATTGAG 1512
333 GlnAlaPheGluIleSerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThr 352
1513 CCACACTTTACGTCACCTTTATGGCACTAATGCAATTCAGACTCTGCCACTGGAA 1572
353 LeuProGlu---ValSerThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAsp 371
1573 ATAGTGGAGCGGATCGAGCAGATGCCACCAACACCTTCTGTGTCTACACCGAGGAGAC 1632
372 IleGlyGluLeuLeuMetLeuLysLeuLysTyrLysSerAspSerTyrPheSerTrpSer 391
1633 TTGGGAGACCTCTTTGAAGATCCAGCTCACTCTGGAGGGGGCTCTCAG---TCTTGTATC 1689
392 AspTrpTrpSer-----SerProGly-----Phe 399
1690 AACCTGTGGAGGAGTTTCGACGACTGCTGTCTCAACCCCGCAACCCCGGAGGAGCTG 1749

400 AlaIleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSer 419
1750 AATATCAGGCGCATCCGGTGAAGTCTGGGGAACCCAGCGGAACCTGACATTTTGTACA 1809
420 ArgGluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHis 439
1810 GAAGACCTGAGAACACACGACATATCCCGAGCGGAGCTCTGTGTTTCGCAAGTGTGCG 1869
440 Asp 440
1870 GAT 1872
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US-10-319-915-99
; Sequence 99, Application US/10319915
; Publication No. US20040115653A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: MODULATION OF ENDOTHELIAL LIPASE EXPRESSION
; FILE REFERENCE: RTS-0447
; CURRENT APPLICATION NUMBER: US/10/319,915
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 279
; SEQ ID NO 99
; LENGTH: 2227
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (275) ... (1777)
US-10-319-915-99
Alignment Scores:
Pred. No.: 5,99e-129 Length: 2227
Score: 1158.00 Matches: 222
Percent Similarity: 68.44% Conservative: 86
Best Local Similarity: 49.33% Mismatches: 120
Query Match: 48.55% Indels: 22
DB: 17 Gaps: 9
US-10-019-341-3 (1-448) x US-10-319-915-99 (1-2227)
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DB 425 TTTAATCCGCACTCTAAGGCCCCAGAGCAGGAGGGTGTAACTCTCCCTTGTGTGAC 484
QY 34 AlaGluSerValAlaThrCysHisPheAsnHisSerSerLysThrPheMetValIleHis 53
DB 485 AGCAAACTCTAGAAAACCTGTGGCTTCAACATGACAGCCAAACCTTTCATCATTCAT 544
QY 54 GlyTrpThrValThrGlyMetTyrGluSerTrpValProLysLeuValAlaLeuTyr 73
DB 545 GGTATGACCATGATGGCATGTTTGAGAGCTGGCTCATTAACCTTGTATCAGCCCTGAG 604
QY 74 LysArgGluProAspSerAsnValIleValValAspTrpLeuSerArgAlaGlnGluHis 93
DB 605 ATGAGAGAGAAAGATGCTAAGCTGCTGGTGGTTGACTGGCTGCCCTGCATCAGCTG 664
QY 94 TyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAlaArgPheIleAsn 113
DB 665 TACACGGATGACATCAATAACACCGAGGTGGTGGGACAGAGATAGCTGGGATGCTTGAC 724
QY 114 TrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeu 133
DB 725 TGGCTGAGGAGGAGAGAGAGTCTCTCTCTTGGGAACGTTTCACTTGTATGCTACAGCCT 784
QY 134 GlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysLysValAsnArgIleThr 153
DB 785 GGAGCACACGCTGGCTGGATACGCTGACCTGCGCACTTTGTGAAGAGAACACAGTGGCAGATCACT 844
QY 154 GlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSerPro 173

Db 845 GGTCTGGATCCGCGGGTCCCATGTTTGAAGGGGTGGACATCAACAGAAGGCTGTCCCG 904
QY 174 AspAlaAspPheValAspValLeuHisThrPheThrArgGlySerProGlyArgSer 193
Db 905 GACGATGCAGACTTGTGGATGTCCTGCATACCTACACGCTG---TCCTTTGGCTTGAGC 961
QY 194 IleGlyIleGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPheGln 213
Db 962 ATTGGGATTCGATCGCTGTGGGTACATTCATGACATCTATCCCAATGGCGGTACTTCCAG 1021
QY 214 ProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAspVal 233
Db 1022 CCAGGCTGGGATTCATGAT-----GTCACTGGATCTTTGCATATGGAACAATC 1072
QY 234 AspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeuLeu 253
Db 1073 TCAGAGATGGTGAATGGAGCAGCGAGCGGTACACCTCTTTGTGACTCTCTGTGTG 1132
QY 254 AsnGluGluAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLysGly 273
Db 1133 AATCAGGACAAGCCAGCTTTGCCCTTCAGTGCACAGACTCCAGCGCTTCAAAAGGGA 1192
QY 274 LeuCysLeuSerCysArgLysAsnArgCysAsnLeuGlyTyrGluIleAsnLysVal 293
Db 1193 ATCTGCCCTCAGCTGCCGAAGAACGGTTGTAAATACATTGGCTACAACGCCCAAGAAATG 1252
QY 294 ArgAlaLysArgSerSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLysVal 313
Db 1253 AGAAGAGAGAGATAGCAAAATGATTTTAAACCCGGGTGGCATGCCCTTTCAAAGTT 1312
QY 314 PheHisTyrGlnValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsnGln 333
Db 1313 TACCATTACCACTGAAAGTTTCAATGTTCTTACATAACAGTGGGGACACCCAGCCC 1372
QY 334 AlaPheGluIleSerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThrLeu 353
Db 1373 ACCCTCTACATCCCTGATGGTAGCAACACCTTCTTGTACTAGAGGAGACTTG 1432
QY 354 ProGlu---ValSerThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAspIle 372
Db 1433 GTGGAGAAGATTGAGCTGAATGCCACAACACCTTCTTGTACTAGAGGAGACTTG 1492
QY 373 GlyGluLeuMetLeuLysLeuLysTyrLysSerAspSerTyrPheSerTyrSerAsp 392
Db 1493 GGGCATCTCTTGAAGATGCGACTTACCTGGAGGGGGTAGCCCAT---TCTGTGTGCAAC 1549
QY 393 TrpTrp-----SerSerProGly-----PheAla 400
Db 1550 CTGTGGAATGAGTTTCGCAACTACCTGTCTCAACCCAGCAACCCCTCGAGGAGCTGTAC 1609
QY 401 IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
Db 1610 ATCCGGCAATTGCTGTCAATCTGGGGAACCCAGCGCAAGTAGCATTTTGCACTCAA 1669
QY 421 GluLysVal---SerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHis 439
Db 1670 GACCAACGAAAGATAGTACTCTCCCTGGCCAG---GAGCTGTGTTTCAAGTGTAC 1726
QY 440 Asp-----LysSerLeuAsnLysLysSer 447
Db 1727 GATGGCTGGAAATGAAAAACAAACCAAGT 1756

Search completed: October 24, 2004, 21:25:18
Job time : 716 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 17:57:24 ; Search time 4360 Seconds
(without alignments)

3744.266 Million cell updates/sec

Title: US-10-019-341-3

Perfect score: 2385

Sequence: 1 ADQRDFIDIESKFAIRTP.....GKPAVFKCHDKSINKSG 448

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2_1/USPTO_spool/US10019341/runat_22102004_120138_1621/app query.fasta_1.647
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10019341 -CGEN 1 1 3437 -runat_22102004_120138_1621 -NCPU=6 -ICPU=3
-NO.WMAP -LARGQUERY -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

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2: gb_est2:.*
3: gb_hic:.*
4: gb_est3:.*
5: gb_est4:.*
6: gb_est5:.*
7: gb_est6:.*
8: gb_gsl1:.*
9: gb_gsl2:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|------------|--------------------|
| 1 | 2385 | 100.0 | 1427 | 9 AY410289 | AY410289 Homo sapi |
| 2 | 2236.5 | 93.8 | 1424 | 9 AY410291 | AY410291 Mus muscu |
| 3 | 2233.5 | 93.6 | 1950 | 3 AK086023 | AK086023 Mus muscu |
| 4 | 2233.5 | 93.6 | 2018 | 3 AK045064 | AK045064 Mus muscu |
| 5 | 2233.5 | 93.6 | 2054 | 3 AK003645 | AK003645 Mus muscu |
| 6 | 2229.5 | 93.5 | 2018 | 3 AK079446 | AK079446 Mus muscu |
| 7 | 2218.5 | 93.0 | 1899 | 3 AK017272 | AK017272 Mus muscu |
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| 9 | 1553 | 65.1 | 2791 | 3 CR605471 | CR605471 full-leng |

| | | | | | | |
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| 10 | 1534 | 64.3 | 1063 | 1 | AL539198 | AL539198 |
| 11 | 1463 | 61.3 | 1076 | 5 | BX418566 | BX418566 |
| 12 | 1388 | 58.2 | 877 | 7 | CF551983 | CF551983 |
| 13 | 1280 | 53.7 | 812 | 7 | CO734715 | CO734715 |
| 14 | 1274.5 | 53.4 | 896 | 4 | BI599196 | BI599196 |
| 15 | 1259.5 | 52.8 | 800 | 7 | CO557716 | CO557716 |
| 16 | 1259 | 52.8 | 758 | 7 | CK359169 | CK359169 |
| 17 | 1253 | 52.5 | 776 | 7 | CK479340 | CK479340 |
| 18 | 1248 | 52.3 | 735 | 7 | CK359202 | CK359202 |
| 19 | 1229.5 | 51.6 | 835 | 4 | BI453917 | BI453917 |
| 20 | 1226 | 51.4 | 721 | 7 | CK355806 | CK355806 |
| 21 | 1205 | 50.5 | 965 | 5 | BQ926353 | BQ926353 |
| 22 | 1190 | 49.9 | 942 | 7 | CF408927 | CF408927 |
| 23 | 1171 | 49.1 | 938 | 5 | BX441464 | BX441464 |
| 24 | 1147 | 48.1 | 768 | 2 | BE911230 | BE911230 |
| 25 | 1138.5 | 47.7 | 772 | 4 | BG429264 | BG429264 |
| 26 | 1130 | 47.4 | 657 | 6 | CB442273 | CB442273 |
| 27 | 1107 | 46.4 | 645 | 5 | BQ695136 | BQ695136 |
| 28 | 1105 | 46.3 | 744 | 6 | CD104574 | CD104574 |
| 29 | 1088.5 | 45.6 | 844 | 5 | BU470625 | BU470625 |
| 30 | 1087 | 45.6 | 892 | 7 | CF551941 | CF551941 |
| 31 | 1086 | 45.5 | 804 | 1 | AU130815 | AU130815 |
| 32 | 1085 | 45.5 | 825 | 7 | CK313328 | CK313328 |
| 33 | 1085 | 45.5 | 3789 | 3 | AK090224 | AK090224 |
| 34 | 1081.5 | 45.3 | 743 | 7 | CK359159 | CK359159 |
| 35 | 1081.5 | 45.3 | 748 | 7 | CK359075 | CK359075 |
| 36 | 1078 | 45.2 | 775 | 7 | CO739014 | CO739014 |
| 37 | 1068 | 44.8 | 656 | 7 | CF908038 | CF908038 |
| 38 | 1063.5 | 44.6 | 855 | 5 | BU439285 | BU439285 |
| 39 | 1045 | 43.8 | 713 | 7 | CR629292 | CR629292 |
| 40 | 1042.5 | 43.7 | 821 | 1 | AL528812 | AL528812 |
| 41 | 1036 | 43.4 | 1429 | 3 | CR619207 | CR619207 |
| 42 | 1036 | 43.4 | 1445 | 3 | CR612434 | CR612434 |
| 43 | 1036 | 43.4 | 1449 | 3 | CR590311 | CR590311 |
| 44 | 1033 | 43.3 | 1396 | 3 | CR596048 | CR596048 |
| 45 | 1027.5 | 43.1 | 957 | 4 | BG176038 | BG176038 |

ALIGNMENTS

| | | | | | | |
|-----------|--|--|---------|-----|--------|-----------------|
| RESULT 1 | AY410289 | Homo sapiens LPL gene, VIRTUAL TRANSCRIPT, partial sequence, | 1427 bp | DNA | linear | GSS 16-DEC-2003 |
| AY410289 | AY410289 | Genomic survey sequence. | | | | |
| VERSION | AY410289.1 | GI:39766257 | | | | |
| KEYWORDS | GSS. | | | | | |
| SOURCE | Homo sapiens (human) | | | | | |
| ORGANISM | Homo sapiens | | | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | | |
| AUTHORS | Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. | | | | | |
| TITLE | 1 (bases 1 to 1427) | | | | | |
| JOURNAL | Science 302 (5652), 1960-1963 (2003) | | | | | |
| PUBMED | 14671302 | | | | | |
| REFERENCE | 2 (bases 1 to 1427) | | | | | |
| AUTHORS | Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. | | | | | |
| TITLE | Direct Submission | | | | | |
| JOURNAL | Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA | | | | | |
| COMMENT | This sequence was made by sequencing genomic exons and ordering them based on alignment. | | | | | |
| FEATURES | Location/Qualifiers | | | | | |
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| Best Local Similarity: | 100.00% |
| Query Match: | 100.00% |
| DB: | 9 |
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| DB | 82 GCGGACCAAGAGAGATTTTATCGACATCGAAAGTAAATTTGCCCTAAGGACCCCTGAA 141 |
| QY | 21 AspThrAlaGluAspThrCysHisLeuLeuProGlyValAlaGluSerValAlaThrCys 40 |
| DB | 142 GACACAGCTGGAGACACTTGCACCTCATCTCCGAGTAGCAGAGTCCGTGGCTACCTGT 201 |
| QY | 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyThrValThrGlyMet 60 |
| DB | 202 CATTTCAATCAGCAGCAAAACCTTCATGGTGATCCATGGCTGGACGGTAAACGGAATG 261 |
| QY | 61 TyrGluSerTrpValProLysLeuValAlaLeuTyrLysArgGluProAspSerAsn 80 |
| DB | 262 TATGAGAGTTGGTGGCAAAACTTGTGGCGGCCCTGTACAAGAGAGAACACGACTCCAAAT 321 |
| QY | 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100 |
| DB | 322 GTCATTGGTGGAGCTGGCTGTCACGGCTCAGGAGCATTTACCATGTGCCGGGGCTAC 381 |
| QY | 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluPheAsn 120 |
| DB | 382 ACCAACTGGTGGACAGAGATGTGGCCCGCTTTATCACTGGATGGAGGAGGTTTAAAC 441 |
| QY | 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaGlyIle 140 |
| DB | 442 TACCTCTGGACAATGCCATCTCTTGGGATACAGCTTGGAGCCCATGCTGCTGGCAT 501 |
| QY | 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160 |
| DB | 502 GCAGGAAGTCTGACCAANTAGAAAGTCAACAGAAATTTACTGGCTCCATCCAGCTGGACCT 561 |
| QY | 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180 |
| DB | 562 AACTTTGAGTATGCAGAGCCCGAGTGGTCTTCTCTGATGATGCAGATTTTGTAGAC 621 |
| QY | 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyLeuGlnLysProVal 200 |
| DB | 622 GTCTTACACATTTACACAGAGGTCCCTGGTGGAGCAATTTGGAATCCAGAAACAGTT 681 |
| QY | 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220 |
| DB | 682 GGCATGTTGACATTTACCCGATGAGGATCTTTTCAGCCAGAGATGATACATTTGGAGAA 741 |
| QY | 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240 |
| DB | 742 GCTATCCGCTGATTTGCAGAGAGAGACTTGGAGATGTGGACCAAGCTAGTGAAGTGCTCC 801 |
| QY | 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluLeuAsnProSerLys 260 |
| DB | 802 CACGAGCGCTCCATTCATCTCTTCATCGACTCTCTGTGTGAATGAAGAAATCCAAATPAG 861 |
| QY | 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280 |
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| QY | 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys 300 |
| DB | 922 AACCGCTGCAACAATCTGGGCTATGAGATCAATTAAGTCAGAGCCCAAGAGAGCAAA 981 |
| QY | 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320 |
| DB | 982 ATGTACCTGAAGACTCGTTCTCAGATGCCCTACAAAGTCTTCCATTACCAAGTAAGATT 1041 |
| QY | 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340 |
| DB | 1042 CATTTTCTGGAGCTGAGAGTGAACCCATACCAATCAGGCTTTGAGATTCTCTGTAT 1101 |
| QY | 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360 |
| DB | 1102 GGCACCGTGGCGAGAGTGAGAACATCCATTCATCTGCCCTGAAGTTCCACAATAAG 1161 |
| QY | 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeu 380 |
| DB | 1162 ACATACCTCTTCTTAATTTACACAGAGGTAGATATTGGAGAACTACTCATGTGAAGCTC 1221 |
| QY | 381 LysTrpLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerProGlyPheAla 400 |
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| QY | 401 IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420 |
| DB | 1282 ATTCAAGAGATCAGAGTAAAGCAGAGAGAGACTCAGAAAAGTGATCTTCTGTCTTAG 1341 |
| QY | 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440 |
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| QY | 441 LysSerLeuAsnLysLysSerGly 448 |
| DB | 1402 AAGTCTCTGAATAAGAAGTCAGGC 1425 |
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| MUS musculus LPL gene, VIRTUAL TRANSCRIPT, partial sequence, | |
| genomic survey sequence. | |
| ACCESSION AY410291.1 GI:39766259 | |
| VERSION AY410291 | |
| KEYWORDS GSS. | |
| SOURCE Mus musculus (house mouse) | |
| ORGANISM Mus musculus | |
| REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | |
| AUTHORS 1 (bases 1 to 1424) | |
| Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A., | |
| Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., | |
| Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., | |
| Adams,M.D. and Cargill,M. | |
| TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous | |
| gene trios | |
| JOURNAL Science 302 (5652), 1960-1963 (2003) | |
| PUBMED 14671302 | |
| REFERENCE 2 (bases 1 to 1424) | |
| Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A., | |
| Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., | |
| Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., | |
| Adams,M.D. and Cargill,M. | |
| AUTHORS Direct Submission | |
| TITLE Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, | |
| Rockville, MD 20850, USA | |
| COMMENT This sequence was made by sequencing genomic exons and ordering | |
| them based on alignment. | |
| FEATURES Location/Qualifiers | |
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ORIGIN

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| DB: | 9 | Gaps: | 1 |

US-10-019-341-3 (1-448) x AY410291 (1-1424)

QY 1 AlaAspGlnArgArgAspPheIleAepIIleGluSerLysPheAlaLeuArgThrProGlu 20
|||||
Db 82 GCAGACGCAGGAAGAGATTCTCAGACATCGAAAGCAAAATTTGCCCTTAGACCCTTGAA 141

QY 21 AspThrAlaGluAspThrCystHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
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QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTrpThrValThrGlyMet 60
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QY 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrlsArgGluProAspSerAsn 80
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Db 262 TATGAGAGTTGGTGCCCNAACTTGTGGCCGCCCTGTACAAGAGAGAACCCTGACTCCAAT 321

QY 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrlsProValSerAlaGlyTyrls 100
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QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrlsSerLeuGlyValaHisAlaGlyIle 140
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QY 161 AsnPheGluTyrlsAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
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Db 802 CATGAGCGCTCATTCATCTCTTCAATTGACTCCCTGTGTAATGAAGAAAAACCCAGCAA 861

QY 261 AlaTyrlsCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
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Qy 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
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RESULT 4
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 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 4
 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 MEDLINE 11076861
 PUBMED 11076861
 5
 The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

REFERENCE
AUTHORS

6 (bases 1 to 2018)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshinori Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. Tomohiro Kono (Department of Animal Science, Tokyo University of Agriculture, 1737 Hunko Aisugi City, Kanagawa Prefecture, Japan) whose assistance we gratefully acknowledge.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/.

FEATURES
source

1..2018
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CDS

88..1512
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ORIGIN

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 Best Local Similarity: 93.53% Mismatches: 17
 Query Match: 93.65% Indels: 1
 DB: 3 Gaps: 1

US-10-019-341-3 (1-448) x AK045064 (1-2018)

Qy 1 AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
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Qy 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
Db 229 GACACAGCTGAGGACACTTGTCTCATCTCTGATTCAGATTCAGAGACTCTGTCTCAACTGC 288
Qy 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTyrThrValThrClyMet 60
Db 289 CACTTCAACACACAGCAGCAACCTTCGTGTGTATCCATGATGAGACGGTAACGGGAATG 348
Qy 61 TyrGluSerTyrValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80
Db 349 TATGAGAGTTGGGTGCCCAACTTGTGGCGCCCTGTACAGAGAGAACTGACTCCCAAT 408
Qy 81 ValIleValValAspTyrLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
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Db 469 ACCAAGCTGGTGGGAAATGATGTGGCCAGATTTCATCACTGGATGGAGAGAGTTTAAC 528
Qy 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyIle 140
Db 529 TACCCCTTAGACAAGCTCCACTCTTAGGGTACAGCCTTGAGCCCATGCTGCTGGCTA 588
Qy 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
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Qy 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
Db 649 AACTTTGATGATGACAGAGCCCCAGTGCCTTTCTCTGATGAGCTGATTTGTAGAT 708
Qy 181 ValLeuHisThrPheArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
Db 709 GTCTTACACACATTACACAGGGGGTCACTGGTGCAGATTATGGAATCCAGAAACAGTA 768
Qy 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
Db 769 GGGCATGTTGACATTATATCCCAATGGAGCACTTTCCAGCCAGGATGCAACATTGGAGAA 828
Qy 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
Db 829 GCATCCGTGTGATTCAGAGAGAGACTCGGAGACGTGGACAGCTGGTGAAGTGTCTG 888
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Db 1009 AATCGCTGTACAAATCTGGCTATGAGATCAACAGGTCTAGAGCCAGAGAGAGCAGCAAG 1068
Qy 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
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Db 1369 ATCAGAGGATCCGAGTGAAGCCGAGAGACTCAGAAAAGGTCTATCTTCTGCTAGG 1428
Qy 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
Db 1429 GAGAAAGTTTCTCATCTCTGCAGAGGAAAGGACTCAGCAGTGTGTTGTGAAATGCCATGAC 1488
Qy 441 LysSerLeuAsnLysLysSerGly 448
Db 1489 AAGTCTCTG---AAGAGTCTGGC 1509

RESULT 5
AK002645 2054 bp mRNA linear HTC 03-APR-2004
LOCUS Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610017C21 product:lipoprotein lipase, full insert sequence.
DEFINITION AK002645 GI:12832782
VERSION AK002645.1
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.
AUTHORS High-efficiency full-length cDNA cloning
TITLE Meth. Enzymol. 303, 19-44 (1999)
JOURNAL 99279253
MEDLINE 10349636
PUBMED
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Tanaka, T., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
PUBMED 11076861
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)

REFERENCE
AUTHORS

6 (bases 1 to 2054)
 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
 Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,
 Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,
 Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,
 Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,
 Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,
 Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
 Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,
 Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,
 Tejima, Y., Toyota, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
 Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 Please visit our web site (http://genome.gsc.riken.jp/) for further
 details.

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN,
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues. First strand cDNA was primed with a primer
 [5'. GAGAGAGCGCGCCACTGAGTCTTTTCTTTTNN 3'], cDNA was
 prepared by using trehalose thermo-activated reverse transcriptase
 and subsequently enriched for full-length by cap-trapper. cDNA went
 through one round of normalization to Rot = 5.0. Second strand cDNA
 was prepared with the primer adapter of sequence [5'.
 GAGAGAGAGGATCCAGAGCTCAATATTTAATTAACCCCCCCCC 3']. cDNA was
 cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end:
 XhoI. Host: SOLR.

FEATURES

Location/Qualifiers
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 /tissue_type="kidney"
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CDS

125..1549
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 DSLIENPNSKAYRCSKEAFKGLCSCKRNKCNILGYEINKVKRKSRLMYLTKRS
 OMPYKVFHYQVHKIFSGTDEGKHOQAFESILGYTVAESENIPFTLPEVSTNKTYSFL
 IYTEVDIGELMLMKLWISDSYFSPMDWSSPSFVIERIRVKAGETQKKVIFCAREKV
 SHLQKGDSDAVFVKCHKSLKKSQ"

ORIGIN

Alignment Scores:

| Pred. No.: | 6.01e-247 | Length: | 2054 |
|------------------------|-----------|---------------|------|
| Score: | 2233.50 | Matches: | 419 |
| Percent Similarity: | 95.98% | Conservative: | 11 |
| Best Local Similarity: | 93.53% | Mismatches: | 17 |
| Query Match: | 93.65% | Indels: | 1 |
| DB: | 3 | Gaps: | 1 |

US-10-019-341-3 (1-448) x AK002645 (1-2054)

QY 1 AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
 Db 206 GCAGACGCGGAGAGAGATTTCTCAGACATCGAAGCAAAATTTGCCCTTAAGACCCCTGAA 265

QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyLeuAlaGluSerValAlaThrCys 40
 Db 266 GACACAGCTGAGGACACTTGTCTCATCTCATCTCTGATTAGACAGACTCTGTCTAATGTC 325

QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyThrThrValThrGlyMet 60
 Db 326 CACTTCAACACACAGCAGCAAGACCTTCTGTGTGATCCATGATGCGGTAACCGGAATG 385

QY 61 TyrGluSerTyrValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80
 Db 386 TATGAGAGTTGGTGCCCAAACTTGTGGCGCCCTGTCAAGAGAGAACTGACTGCTCAAT 445

QY 81 ValIleValValAspTyrLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
 Db 446 GTCAATTGTAGTAGACTGTGTGTATCGGCGCCAGCAACATTATCCACTGTGCTGCTGCTAC 505

QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTyrMetGluGluPheAsn 120
 Db 506 ACCAAGCTGTGGGAAATGATGTGCCAGATTATCACTGATGAGGAGGAGGAGTTTAAAC 565

QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyValAlaHisAlaGlyIle 140
 Db 566 TACCCCTTAGACAAAGTCCACCTCTTAGGTACAGCTTTGGAGCCCTGCTGCTGCTGCTA 625

QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
 Db 626 GCAGGAAGTCTGACCAATAAGAAAGTCAATAGTAATTTACTGTTTGGATCCAGTGGCT 685

QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
 Db 686 AACTTTGAGTATGCAGAACCCCGCTGCTCTCTCTGATGACGCTGATTTGTAGAT 745

QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
 Db 746 GTCTTACACACATTTACAGGGGGTCACTGTGTGCAAGTATTGGAAATCCAGAAACAGTA 805

QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
 Db 806 GGGCATGTTGACATTTATCCCAATGGAGGCACTTTCCAGCCAGGATGCAACATTGGAGAA 865

QY 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
 Db 866 GCCATCCCGTGTGATTCAGAGAGAGAGGACTCGAGACGTGGACCTGCTGAAAGTCTCG 925

QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluAsnProSerLys 260
 Db 926 CACGAGCGCTCCATTCATCTCTTATGACTCCCTGCTGAATGAAGAAACCCAGCAAG 985

QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
 Db 986 GCATACAGTGCACACTCCAGGAAGGCTTTGAGAAAGGGCTCTGCTGAGTTGTAGAAAG 1045

QY 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys 300
 Db 1046 AATCGCTGTAACTATGGGCTATGAGATCAACAAGGTGAGAGCAAGAGAGAGCAAG 1105

QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
 Db 1106 ATGTACCTGAAGACTCCCTCTCAGATCCCTTACAAAGTGTTCATTACCAAGTCAAGAT 1165

QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
 Db 1166 CACTTTTCTGGGACTGAGGATGGCAACCAACACAGCCCTTCGAGATTCTCTGTAC 1225

QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360

| | | | | | | |
|-----------|---|---|-----------|---|--|--|
| 1226 | GGCACAGTGGCCGAGAGCGAGAACATTCCTTTCCCTCCCGAGGTTTCCACAAATAAA | 1285 | REFERENCE | 6 (bases 1 to 2018) | AUTHORS | Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nomura, K., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. |
| 361 | ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeu | 380 | JOURNAL | Submitted (16-APR-2002) | Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216) | |
| 1286 | ACCTACTCTCTTCTGATTACACGAGGTGGACATCGGAGAACTGCTCATGATGAAGCTT | 1345 | COMMENT | CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. | Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers 1. .2018 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM_DB:9930034G02" /db_xref="taxon:10090" /clone="9930034G02" /sex="female" /tissue_type="vagina" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult" 88. .1512 /note="unnamed protein product; lipoprotein lipase (MGD [MGI:96820]) putative" /codon_start=1 /protein_id="BAC37646.1" /db_xref="GI:26347995" /translation="MEEKALLLVLVGVWVLSQSLTAFRGVAAEDAGDFSDIESKFAIRTPEDTAEDTCHLIPGLADSVSNCHFNHSSKTFVHGWTVTGMYSWPKLVAAVLYKRSGITQGVGHVIVPNPGTTPGCGNIGVAGTATGAGNFEVFAEAPSRISPDADFVDVHLFTFTGSPQVADSLNNEENPDKAYRCNCEAFEGKFCSCRKNRNNGEYKINLVKRAKSSKSKYLLKTSQMLYKVFHVQVKTPEDEGKHQNAFETISLYGVAESENIPFTLPEVSTNKTYSIFLITVEYDICELLMMKLKWTSDSYFVSWPDMWSSPSFVIERIRVKGAGETQKKVIFCAREKVS | |
| 381 | LysTrpLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerSerProGlyPheAla | 400 | FEATURES | source | 1.7e-246 Length: 2018 Pred. No.: 2229.50 Score: 418 Percent Similarity: 95.97% Best Local Similarity: 93.51% Query Match: 93.48% DB: 3 US-10-019-341-3 (1-448) x AK079446 (1-2018) | |
| 1346 | AAGTGGATAAGCGACTCTCTACTTCAGCTGGCTGACTGGTGAGAGAGCCCGCCAGCTTC | 1405 | ORIGIN | Alignment Scores: | 20530913 Genome Res. 10 (11), 1757-1771 (2000) 11076861 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001) The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) | |
| 401 | IleGlnLysIleArgValIleAlaGlyGluThrGlnLysLysValIlePheCysSerArg | 420 | REFERENCE | 2 | Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. | |
| 1406 | ATCGAGAGATCCCGAGTGAAGCCGAGAGACTCAGAAAGGCTCATCTTCTGTGCTAGG | 1465 | TITLE | High-efficiency full-length cDNA cloning | Meth. Enzymol. 303, 19-44 (1999) | |
| 441 | LysSerLeuAsnLysLysSerGly | 448 | JOURNAL | Genome Res. 10 (10), 1617-1630 (2000) | Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. | |
| 1526 | AAGTCTCTG---AAGAAGTCTGGC | 1546 | REFERENCE | 3 | Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. | |
| RESULT 6 | AK079446 | 2018 bp mRNA linear HTC 03-APR-2004 | TITLE | Normalisation and subtration of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes | Genome Res. 10 (10), 1617-1630 (2000) | |
| ACCESSION | AK079446.1 | GI:26347994 | JOURNAL | Genome Res. 10 (10), 1617-1630 (2000) | Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. | |
| VERSION | HTC; CAP trapper. | | JOURNAL | Genome Res. 10 (10), 1617-1630 (2000) | Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. | |
| KEYWORDS | Mus musculus (house mouse) | | JOURNAL | Genome Res. 10 (10), 1617-1630 (2000) | Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. | |
| SOURCE | Mus musculus | | JOURNAL | Genome Res. 10 (10), 1617-1630 (2000) | Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. | |
| ORGANISM | Mus musculus | | JOURNAL | Genome Res. 10 (10), 1617-1630 (2000) | Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. | |
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| AUTHORS | Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. | Normalisation and subtration of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes | JOURNAL | Genome Res. 10 (10), 1617-1630 (2000) | Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. | |
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| MEDLINE | 20530913 | 11076861 | JOURNAL | Genome Res. 10 (10), 1617-1630 (2000) | Shibata, K., Itoh, M., | |

QY 22 ThrAlaGluAspThrCysHisLeuLeuProGlyValAlaGluSerValAlaThrCysHis 41
 Db 232 ACAGCTGAGGACACTTGTCTATCTCATCTCTGGATTAGACAGACTCTGTCTTAAGTGCAC 291
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 QY 442 SerLeuAsnLysLysSerGly 448
 Db 1492 TCTCTG---AAGAAGTCTGGC 1509
 RESULT 7
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 DEFINITION
 Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430405H20 product:Lipoprotein lipase, full insert sequence.
 AK017272
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
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81 ValIleValValAspTyrLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
 518 GTCAATTTAGTAGACTGGTTGTATCGGGCCAGCAATATTCAGTGTAGCTGGCTAC 577
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 1538 GAGAAAGTTTCTCATCTGCAGAGGAAAGGACTCAGCAGGTGTTTGTGAATGC 1597
 441 LysSerLeuAsnLysLysSerGly 448

TITLE
 JOURNAL
 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 please visit our web site (http://genome.gsc.riken.jp/) for further
 details.

CDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues. First strand cDNA was primed with a primer
 [5', GAGAGAGAGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was
 prepared by using trehalose thermo-activated reverse transcriptase
 and subsequently enriched for full-length by cap-trapper. cDNA went
 through one round of normalization to Rot = 10.0 and subtraction to
 Rot = 100.0. Second strand cDNA was prepared with the primer
 adapter of sequence [5',
 GAGAGAGAGATCTCGAGTTAAATTAATCCGCCGCCGCC 3']. cDNA was cleaved
 with BamHI and XhoI. Vector: a modified pBluescript KS(+) after
 bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3',
 end: BamHI. Host: DH10B.
 Location/Qualifiers
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 197. .1621
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 putative"

FEATURES

source

ORIGIN

Alignment Scores:
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 Percent Similarity: 95.76% Conservative: 11
 Best Local Similarity: 93.30% Mismatches: 18
 Query Match: 93.02% Indels: 1
 DB: 3 Gaps: 1
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 QY 1 AlaAspGlnArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
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 QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
 DB 338 GACACAGCTGAGGACACTTGTCTATCTCTCTGATTTAGCAGACTCTGTGTCTAACTGC 397
 QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTyrThrValThrGlyMet 60
 DB 398 CACTTCAACCAACAGACAGAACCTTCTGCTGATCATGATGATGACCGTAAACGGAATG 457
 QY 61 TyrGluSerTyrValProLysLeuValAlaLeuTyrLysArgGluProAspSerAsn 80
 DB 458 TATGAGAGTTAGTCCCAAACTTGTGGCCGCCCTGTACAGAGAGAGAACCTGACTCCAAT 517

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Db      1598 AAGTCTCTG---AGAGAGCTGGC 1618
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RESULT 8
LOCUS   AY410290
DEFINITION Pan troglodytes LPL gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY410290
VERSION   AY410290.1 GI:39766258
KEYWORDS  GSS.
SOURCE    Pan troglodytes (chimpanzee)
ORGANISM  Pan troglodytes
REFERENCE 1 (bases 1 to 1427)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED    14671302
REFERENCE 2 (bases 1 to 1427)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE     Direct Submission
JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering them based on alignment.
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gene
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Pred. No.:      6.67e-201      Length:      1427
Score:          1834.00      Matches:    356
Percent Similarity: 79.69%      Conservative: 1
Best Local Similarity: 79.46%      Mismatches: 91
Query Match:    76.90%      Indels:    0
DB:              9      Gaps:      0

US-10-019-341-3 (1-448) x AY410290 (1-1427)
Qy      1 AlaAspGlnArgAspPheileAspIleGluSerLysPheAlaLeuArgThrProGlu 20
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Db      82 GCCGACCCNNNNNNNGATTTTATGACATGAAAGTAAATTTGCCCTANNNNNCCCTGAN 141
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Qy      61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80
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Qy      81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
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Qy      101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluPheAsn 120
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Qy      121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaGlyIle 140
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Qy      141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
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Qy      161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
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Db      562 AACCTTGGATGATGAGAACGCCCGAGTCGCTTTCTCTGATGATGACAGATTTTGTAGAT 621
Qy      181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
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Qy      201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
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Qy      221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
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Qy      241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
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Qy      261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
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Db      862 GCCTACAGGTGCAGTTCACAGGAAGCCCTTCAGAAAGGGCTCTGCTCAGTTGTAGAAG 921
Qy      281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys 300
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Db      922 AACCGCTGCAACAATCTGGGCTATCAGATCAATAAAGTCAGAGCCAAAGAGCAGCAA 981
Qy      301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
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Db      982 ATGTACCTGGAAGCTCGTTCTCAGATGCCCTTACAAAGCTTCCCATTAACAAGTAAGATT 1041
Qy      321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
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Db      1042 CATTTTCTGGGACTGAGAGTGAAACCCATACCAACCCAGGCTTTGAGATTTCTCTGTAT 1101
Qy      341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
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Qy      381 LysTrpLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerSerProGlyPheAla 400
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Qy      401 IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
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Qy      421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
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Qy      441 LysSerLeuAsnLysLysSerGly 448
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RESULT 9
CR605471 2791 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DF034YK01 of Fetal brain of Homo sapiens
DEFINITION (human).
ACCESSION CR605471
VERSION CR605471.1 GI:50486278
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue
2 (bases 1 to 2791)
REFERENCE
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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Score: 1553.00 Matches: 292
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 65.12% Indels: 0
DB: 3 Gaps: 0
US-10-019-341-3 (1-448) x CR605471 (1-2791)
QY 157 ProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAla 176
Db 3 CCAGCTGGACCTAACTTTGAGTATCGAAGCCCGAGTCGCTTTCTCTGATGATGCA 62
QY 177 AspPheValAspValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyTyr 196
Db 63 GATTTGTAGAGCTTTACACATTCACCAGAGGGTCCCTGGTGGAGCATTTGGATC 122
QY 197 GlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCys 216
Db 123 CAGAAACCATGTTGGGCATGTTGACATTTACCCGAATGGAGGTACTTTTCAGCCAGGATGT 182
QY 217 AsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeu 236
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QY 237 ValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGlu 256
Db 243 GTGAAGTGTCTCCACGAGGCGCTCCATTCATCTTCATCGACTCTCTGTGATGAAGNA 302
QY 257 AsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluGlyGlyLeuCysLeu 276
Db 303 AATCCAAGTAAGGCCTACAGGTGCAGTTCCAAAGGAAGCCTTTGAGAAAGGGCTCTGCTTG 362

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QY 277 SerCysArgLysAsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLys 296
Db 363 AGTTGTAGAAAGAACCGCTGCAACAATCTGGCTATGAGATCAATAAAGTCAGAGCCAAA 422
QY 297 ArgSerSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyr 316
Db 423 AGAAGCAGCAAAATGTACTGAGACTGTTCTCAGATGCCCTACAAAGTCTTCCATTAC 482
QY 317 GlnValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGlu 336
Db 483 CAAGTAAAGATTCAATTTCTGGGACTGAGAGTGAACCCATACCAATCAGGCCCTTTGAG 542
QY 337 IleSerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluVal 356
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QY 357 SerThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeu 376
Db 603 TCCACAAATAGACCTACTCTCTCTAATTTACACAGAGGTAGATATTGGAGAACTACTC 662
QY 377 MetLeuLysLysLysTyrPheSerAspSerTyrPheSerTyrPheSerAspTyrTrpSerSer 396
Db 663 ATGTTGAAGCTCAAAATGAAGAGTGAATTCATCTTAGCTGCTCAGACTGGTGGAGCAGT 722
QY 397 ProGlyPheAlaIleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIle 416
Db 723 CCCGCTTCGCGCATTCAGAAATCAGAGTAAAGCAGAGAGACTCAGAAAAGGTGATC 782
QY 417 PheCysSerArgGluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheVal 436
Db 783 TTTCTGTTCTAGGAGAAAGTGTCTCATTTGCAGAAAGGAAGGCACCTGGGTATTGTG 842
QY 437 LysCysHisAspLysSerLeuAsnLysLysSerGly 448
Db 843 AAATGCCATGACAAAGTCTCTGAATAAGAAAGTCAGGC 878
RESULT 10
AL539198 1063 bp mRNA linear EST 24-MAR-2004
LOCUS AL539198 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DF034YK01 5-PRIME, mRNA sequence.
ACCESSION AL539198
VERSION AL539198.3 GI:45714871
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31263768.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 4684.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DF034YK01&c=4684.f.
FEATURES
source
1.1063 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF034YK01"
/tissue_type="FETAL BRAIN"

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/dev_stage="fetal"
 /clone_lib="Homo sapiens FETAL BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Alignment Scores:

Pred. No.: 2,44e-166 Length: 1063
 Score: 1534.00 Matches: 291
 Percent Similarity: 99.32% Conservative: 0
 Best Local Similarity: 99.32% Mismatches: 1
 Query Match: 64.32% Indels: 1
 DB: 1 Gaps: 0

US-10-019-341-3 (1-448) x AL539198 (1-1063)

QY 157 ProAlaGlyProAsnGlyHisValAspLeuSerArgLeuSerProAspAla 176
 DB 3 CCAGCTGGAGCTTAACCTTGTAGTATGACAGAGCCCCGAGTCTCTTCTCTGATGATGCA 62
 QY 177 AspPheValAspValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIle 196
 DB 63 GATTTTGTAGAGCTCTTACACATTCACAGAGGGTCCCTCGTGAAGCATTTGAATC 122
 QY 197 GlnLysProValGlyHisValAspLeuSerArgLeuSerGlyThrPheGlnProGlyCys 216
 DB 123 CAGAACCAAGTGGGCAATGTTGACATTTACCCGATGGGGTACTTTTCAGCCAGCATGT 182
 QY 217 AsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeu 236
 DB 183 AACATTGGAGAGCTATCCGCTGATTTGACAGAGAGGACTTGGAGATGTGGACCACTA 242
 QY 237 ValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGlu 256
 DB 243 GTGAAGTGTCTCCACAGAGCGCTCCATTCATCTCTTCAGTACTCTGTTGAATGAGNA 302
 QY 257 AsnProSerLysAlaTyArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeu 276
 DB 303 AATCCAGTAAAGCTTACAGGTGCGAGTCCAAAGGAGCGCTTTGAGAAAGGGCTCTGCTG 362
 QY 277 SerCysArgLysAsnArgCysAsnLeuGlyTyGluIleAsnLysValArgAlaLys 296
 DB 363 AGTTGTAGAAAGAACCGCTGCAACATCTGGCTATGATGATCAATAAAGTCAGACCCAAA 422
 QY 297 ArgSerLysMetTyLeuLysThrArgSerGlnMetProTyLysValPheHisTyI 316
 DB 423 AGAAGCAGCAAAATGTACTGAAGACTCGTTCTCAGATGCCCTACAAAGTCTTCCATTAC 482
 QY 317 GlnValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGlu 336
 DB 483 CAAGTAAAGATTCATTTCTGGAGCTCAGAGTGAACCCATACCAATCAGCGCTTTCAG 542
 QY 337 IleSerLeuTyGlyThrValAla-GluSerGluAsnIleProPheThrLeuProGluVa 356
 DB 543 ATTTCTCTGTATGACCGCTGGCGAGAGTGAGACATCCCATTCATCTCTGCTGAGT 602
 QY 356 lSerThrAsnLysThrTySerPheLeuIleTyThrGluValAspIleGlyGluLeuLe 376
 DB 603 TTCCACAAATWAGACCTACTCTCTTCTTAATTTACACAGAGGTAGATATTGGAGAACTACT 662
 QY 376 uMetLeuLysLeuLysTrpLysSerAspSerTyPheSerTrpSerAspTrpTrpSerSe 396
 DB 663 CATGTTGAGCTCAATGGAAGATGATTCATCTTTAGCTGGTGGAGAGTGGAGCAG 722
 QY 396 rProGlyPheAlaIleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValI 416
 DB 723 TCCGGCTTCGCCATTTCAGAGATCAGAGTAAAGCAGGAGAGACTCAGAAAAAGGTGAT 782
 QY 416 ePheCysSerArgGlnLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheVa 436

DB 783 CTTCTGTCTAGGAGAAAGTGTCTCATTTGACAAAGAAAGGACCTGGGTATTGT 842
 QY 436 lLysCysHisAspLysSerLeuAsnLysLysSerGly 448
 DB 843 GAAATGCATGACAAAGTCTCTGATAAAGAAAGTCAAGC 879
 RESULT 11
 BX418566
 LOCUS
 DEFINITION BX418566 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 CS0DF007YI16 5-PRIME, mRNA sequence.
 ACCESSION BX418566
 VERSION BX418566.2 GI:46927755
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1076)
 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 13, 2003 this sequence version replaced gi:30642295.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 4684.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?s=CS0DF007BE08QPlsc=4684.f.

FEATURES

source

1..1076
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DF007YI16"
 /tissue_type="FETAL BRAIN"
 /dev_stage="fetal"
 /clone_lib="Homo sapiens FETAL BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Alignment Scores:

Pred. No.: 4,2e-158 Length: 1076
 Score: 1463.00 Matches: 277
 Percent Similarity: 95.59% Conservative: 5
 Best Local Similarity: 93.90% Mismatches: 13
 Query Match: 61.34% Indels: 1
 DB: 5 Gaps: 0

US-10-019-341-3 (1-448) x BX418566 (1-1076)

QY 154 GlyLeuAspProAlaGlyProAsnGlyHisValAspLeuHisThrArgGlySerProGlyArgSer 173
 DB 1 GGCTCGATCCAGCTGGACCTACTTTCAGTATGACAGAGCCCGAGTCGTCTTCTCT 60
 QY 174 AspAspAlaAspPheValAspValLeuHisThrPheThrArgGlySerProGlyArgSer 193
 DB 61 GATGATGCAGATTTCGTAGACGCTTACACACATTCACAGAGGGTCCCTGGTCGAGC 120
 QY 194 IleGlyLleGlnLysProValGlyHisValAspIleTyProAsnGlyGlyThrPheGln 213
 DB 121 ATTGGAATCCAGAAACAGTTGGCATGTTGACATTTACCCGAATGAGGTACTTTTCAG 180

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: NDAM618 row: h column: 05
 High quality sequence stop: 701.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30529996"
 /lab_host="DH10B-Tona (T1 and T5 phage resistant)"
 /clone_lib="NIH MGC 183"
 /note="Organ: Pooled muscle (cardiac and skeletal); Vector: pCMV-SPORT6.1; Site 1: EcoRV (destroyed); Site 2: NotI; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7. Library was constructed by Invitrogen."

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.: 1,49e-149 Length: 877
 Score: 1388.00 Matches: 270
 Percent Similarity: 99.27% Conservative: 1
 Best Local Similarity: 98.90% Mismatches: 2
 Query Match: 58.20% Indels: 2
 DB: 7 Gaps: 0

US-10-019-341-3 (1-448) x CF551983 (1-877)

QY 214 ProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAspVal 233
 Db 181 CCAGATGTAACATTTGGAGAGCTATCCGCGTGATTCAGAGAGAGAGCTTGGAGATGG 240
 QY 234 AspGlnLeuValLysCysSerHisGluArgSerIleHisIleAspSerLeuLeu 253
 Db 241 GACCAGCTAGTGAAGTGTCCACGAGGCTCCATTCATCTCTTCATGACTCTCTTTT 300
 QY 254 AsnGluGluAsnProSerLysAlaIleArgCysSerSerLysGluAlaPheGluLysGly 273
 Db 301 AATAAAAAAATCCAAAGTAGAGCTCAGGTGCACTTCCAGGAGAGCCCTTTGARAAGGG 360
 QY 274 LeuCysLeuSerCysArgLysAsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysVal 293
 Db 361 CTCGCTTGAATTTAGAAAGAACCGCTGCAACAATCTGGGTATGAATCAATAAATC 420
 QY 294 ArgAlaLysArgSerSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLysVal 313
 Db 421 AGAGCCAAAAAAGAGCAGCAAAATGTACCTGGAAGCTCGTTCTCAGATGCCCTTACAAGTC 480
 QY 314 PheHisTyrGlnValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsnGln 333
 Db 481 TTCATTACCAAGTAAGATTCATTTTCTGGACTGAGAGTGAAACCCATACCAATCAG 540
 QY 334 AlaPheGluIleSerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThrLeu 353
 Db 541 GCCTTTAAATTTCTCTGTATGACCGCTGGCGGAGAGTGAGAACAATCCATTCACCTCTG 600
 QY 354 ProGluValSerThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAspIleGly 373
 Db 601 CCGTGAAGTTTCCACAAATAGACCTACTCTCTCTTAATTTACACAGGAGGAGATTTGGA 660
 QY 374 GluLeuLeuMetLeuLysLysTyrLysSerAspSerTyrPheSerTrpSerAspTrp 393
 Db 661 GAACCTACTCATGTTGAAGTCAATGGRAGAGTGATTCATCTTACCTGGKAGAGCTGG 720
 QY 394 TrpSerSerProGlyPheAlaIleGlnLysIleArgValLysAlaGlyGluThrGlnLys 413
 Db 721 TGGRCGAGTCCCGGTTGCG-ATTCAAGATCAGAGTAAATCAAGAGAGAGCTCAGAA 779
 QY 414 LysValIlePheCysSerArgGluLysValSerHisLeuGlnLysGlyLysAlaProAla 433
 Db 780 AAGGTGATCTCTGTTTGGGGGAAAGTGTCTCATTTGAGAAAGRAAGGRCCTGG 839
 QY 434 ValPheValLysCysHisAspLysSerLeuAsnLysLysSerGly 448
 Db 840 GKATTTGTGAATGCCATGACAGTCTCTGAATAAAAGTCAGG 884

RESULT 12

CF551983 877 bp mRNA linear EST 22-SEP-2003
 LOCUS AGENCOURT 15594985 NIH MGC 183 Homo sapiens cDNA clone
 DEFINITION IMAGE:30529996 5', mRNA sequence.

ACCSSION CF551983

VERSION CF551983.1 GI:34888817

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 877)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

176 AlaAspPheValAspValLeuHisThrPheThrArgGlySerProGlyArgSerIleGly 195
 Db 1 GCAGATTTGTAGACGCTTATC-ACATTCACAGAGGGTCCCTGTCGAGCATTTGA 59
 QY 196 IleGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGly 215
 Db 60 ATCCAGAAACCAAGTTGGGCATCTTGACATTTACCCGAATGGAGGTACTTTTCAGCCAGGA 119
 QY 216 CysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGln 235
 Db 120 TGTAAATTTGGAGAGCTATCCCGTGATTCAGAGAGAGAGACTTGGAGATGTGGACAG 179
 QY 236 LeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGlu 255
 Db 180 CTAGTGAAGTGTCTCCACAGAGCGCTCCATTCATCTCTTCATGACCTCTCTGTTGAATGAA 239
 QY 256 GluAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCys 275
 Db 240 GAAAAATCCAAAGTAAGGCTACAGGTGCAGTTCCAAAGGAAGCCCTTTGAGAAAGGCTCTGC 299
 QY 276 LeuSerCysArgLysAsnArgCysAsnLeuGlyTyrGluIleAsnLysValArgAla 295
 Db 300 TTGAGTTGTAGAAAGAACCCCTGCAACAATCTGGCTATGAGATCAATAAGTCAGAGCC 359
 QY 296 LysArgSerSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHis 315
 Db 360 AAAAGAGCAGCAAAATGTACTTCAAGACTCGTTCTCAGATGCCCTCAAAAGTCTTCAT 419
 QY 316 TyrGlnValLysIleHisPheSerGlyThrGlnSerGluThrHisThrAsnGlnAlaPhe 335
 Db 420 TACCAAGTAAAGATTCATCTTTCTGGGACTGAGAGTGAACCCATACCAATCAGGCCTTT 479
 QY 336 GluIleSerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThrLeuProGlu 355
 Db 480 GAGATTTCTGTATGGCACCCTGGCCGAGAGTGAAGCAATCCCATTCACCTCTGCCTGAA 539
 QY 356 ValSerThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeu 375
 Db 540 GTTTCCACAAATAAGACCTACTCTCTTCTTAATTTACACAGAGGTAGATATTGGAGAACTA 599
 QY 376 LeuMetLeuLysLeuLysTyrLysSerAspSerTyrPheSerTrpSerAspTrpTrpSer 395
 Db 600 CTCATGTTGAAGCTCAAAATGGAAGAGTGAATTCATCTTTAGCTGCTCAGACTGGTGGAGC 659

| | | | |
|----|-----|--|-----|
| Qy | 396 | SerProGlyPheAlaIleGlnLysIleArgVallysAlaGlyGluThrGlnLysLysVal | 415 |
| Db | 660 | AGTCCCGGCTTCGCATTCCAGACATCAGATTAAAGCAGAGAGACTTCAGAAAAGGTG | 719 |
| Qy | 416 | IlePheCysSerArgGluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPhe | 435 |
| Db | 720 | ATCTTCTGTTCTAGGGAGAAAGTGTCTCATTTGCAGAAAGCAAGCA-CTTCGGGTATTT | 778 |
| Qy | 436 | VallysCysHisAspLysSerLeuAsnLysLysSerGly | 448 |
| Db | 779 | GTGAATGCCATGACAAAGTCTCTGAATAAGAGTCAGGC | 817 |

| | | | |
|---|--------|---|----------|
| found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LHAM11764 row: b column: 08 High quality sequence stop: 805. | | 1. 896 Location/Qualifiers /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5301799" /tissue_type="hypothalamus" /lab_host="DH10B" /clone_lib="NIH_MGC_96" /note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcagag); Oligo-dT primed using primer 5'-TTTTTTTCTTTTNN-3', size-selected for average insert size 2.3 kb and normalized to 80T 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library." | |
| FEATURES | source | Alignment Scores: | |
| | | Pred. No.: | 2.2e-136 |
| | | Score: | 1274.50 |
| | | Percent Similarity: | 93.40% |
| | | Best Local Similarity: | 92.01% |
| | | Query Match: | 53.44% |
| | | DB: | 4 |
| ORIGIN | | US-10-019-341-3 (1-448) x B1599196 (1-896) | |
| QY | 1 | AlaAspGlnArgGlySerPheAlaLeuArgThrProGlu | 20 |
| DB | 51 | GCGGCAAGAGAGATTTCGACATCGAAGTAATTTGCCCTTAGACCCCTGAA | 110 |
| QY | 21 | AspThrAlaGluAspThrCysHisLeuIleProGly-ValAlaGluSerValAlaThrCy | 40 |
| DB | 111 | GACACAGCTGAGACACTTCCACCTCATTTCCCGAGATAGCAGAGTCCATGCTACCTG | 170 |
| QY | 40 | sHisPheAsnHis-SerSerIysThrPheMetValIleHisGlyThrValThrGlyM | 60 |
| DB | 171 | TCATTTCAATCACAGACAGCAAAACCTTCATGTTGATCCATGCTGACGGTAACAGAA | 230 |
| QY | 60 | etTyrGluSerTrpValProIysLeuValAlaAlaLeuTyrLysArgGluProAspSerA | 80 |
| DB | 231 | TGTATGAGATTGGTGCCAAACTTGTGGCCGCCCTGTACAGAGAACCCAGACTCCA | 290 |
| QY | 80 | snValIleValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyT | 100 |
| DB | 291 | ATGTCATTGTGGTGGCTGGCTGTACAGGCG-CAGGAGCATTTACCCAGTGTCCCGGGCT | 349 |
| QY | 100 | YrThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheA | 120 |
| DB | 350 | ACACCAACTGTGGGACAGGATGGCCCGGTTTATCACTGGATGGAGGAGGATTTA | 409 |
| QY | 120 | snTyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyValaHisAlaAlaGlyI | 140 |
| DB | 410 | ACTACCTCTGGCAATGTCCATCTCTGGGATACAGCCCTTGGAGCCCATGCTGTGGCA | 469 |
| QY | 140 | leAlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAsp-ProAlaGly | 159 |
| DB | 470 | TTGCAGGAAGTCTGACCAATAAGAAAGTCAACAGAAATTAATCTGCTGATGCCAGTGA | 529 |
| QY | 160 | ProAsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAsnAlaAspPheVal | 179 |
| DB | 530 | CCTAACTTGTAGTATGACAGACCCCGAGTGGTCTTCTCTGTGATGTCAGATTTGTA | 589 |
| QY | 180 | AspValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysPro | 199 |
| found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LHAM11764 row: b column: 08 High quality sequence stop: 805. | | 1. 896 Location/Qualifiers /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5301799" /tissue_type="hypothalamus" /lab_host="DH10B" /clone_lib="NIH_MGC_96" /note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcagag); Oligo-dT primed using primer 5'-TTTTTTTCTTTTNN-3', size-selected for average insert size 2.3 kb and normalized to 80T 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library." | |
| FEATURES | source | Alignment Scores: | |
| | | Pred. No.: | 2.2e-136 |
| | | Score: | 1274.50 |
| | | Percent Similarity: | 93.40% |
| | | Best Local Similarity: | 92.01% |
| | | Query Match: | 53.44% |
| | | DB: | 4 |
| ORIGIN | | US-10-019-341-3 (1-448) x B1599196 (1-896) | |
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| DB | 51 | GCGGCAAGAGAGATTTCGACATCGAAGTAATTTGCCCTTAGACCCCTGAA | 110 |
| QY | 21 | AspThrAlaGluAspThrCysHisLeuIleProGly-ValAlaGluSerValAlaThrCy | 40 |
| DB | 111 | GACACAGCTGAGACACTTCCACCTCATTTCCCGAGATAGCAGAGTCCATGCTACCTG | 170 |
| QY | 40 | sHisPheAsnHis-SerSerIysThrPheMetValIleHisGlyThrValThrGlyM | 60 |
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| QY | 80 | snValIleValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyT | 100 |
| DB | 291 | ATGTCATTGTGGTGGCTGGCTGTACAGGCG-CAGGAGCATTTACCCAGTGTCCCGGGCT | 349 |
| QY | 100 | YrThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheA | 120 |
| DB | 350 | ACACCAACTGTGGGACAGGATGGCCCGGTTTATCACTGGATGGAGGAGGATTTA | 409 |
| QY | 120 | snTyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyValaHisAlaAlaGlyI | 140 |
| DB | 410 | ACTACCTCTGGCAATGTCCATCTCTGGGATACAGCCCTTGGAGCCCATGCTGTGGCA | 469 |
| QY | 140 | leAlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAsp-ProAlaGly | 159 |
| DB | 470 | TTGCAGGAAGTCTGACCAATAAGAAAGTCAACAGAAATTAATCTGCTGATGCCAGTGA | 529 |
| QY | 160 | ProAsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAsnAlaAspPheVal | 179 |
| DB | 530 | CCTAACTTGTAGTATGACAGACCCCGAGTGGTCTTCTCTGTGATGTCAGATTTGTA | 589 |
| QY | 180 | AspValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysPro | 199 |

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ORIGIN
Library*

Alignment Scores:
Pred. No.:      1e-134      Length:      800
Score:          1259.50     Matches:    237
Percent Smilarity: 96.84%   Conservative: 8
Best Local Smilarity: 93.68% Mismatches:   7
Query Match:    52.81%     Indels:    1
DB:             7          Gaps:       1

US-10-019-341-3 (1-448) x COS57716 (1-800)

QY 109 AlaArgPheIleAsnTrpMetGluGluPheAsnTyrProLeuAspAsnValHisLeu 128
Db 29 GCCAGGTTTCATCAACTGGTTGGAGGAGAGATTAACTACCCCTAGACAATGCCACCTC 88

QY 129 LeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysLys 148
Db 89 TTAGGGTACAGTCTTGGAGCCCATGCTGCTGGCGTGGCAGGAAGTCTGACCAACAAGAAG 148

QY 149 ValAsnArgIleThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaPro 168
Db 149 GTCAATAGATTAATCTGGCTTGGATCCAGCTGGGCGCTAACTTTGAGTATGCAGAAGCCCT 208

QY 169 SerArgLeuSerProAspAlaAspPheValAspValLeuHisThrPheThrArgGly 188
Db 209 AGTCGCCTTCTCCTCATGATCGGATTTCGTAGATGTCCTACACACATTTACAGGGGG 268

QY 189 SerProGlyArgSerIleGlyIleGlnLysProValGlyHisValAspIleTyrProAsn 208
Db 269 TCGCCCTGGTCGAGATATTGGGATCCAGAAACCAAGTAGGCGCATGTTGATATTTATCCCAAT 328

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Search completed: October 24, 2004, 21:11:26
Job time : 4381 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 17:12:55 ; Search time 6058 Seconds
(without alignments)
3497.158 Million cell updates/sec

Title: US-10-019-341-3
Perfect score: 2385
Sequence: 1 ADORRFIDIESFAIRTFE.....GKAPVFKCHDKSLKSG 448

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | | | | |
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| Result No. | Score | Query Match | Length DB | Description |
| 1 | 2385 | 100.0 | 1612 | 9 HSLIPAS X54516 Human mRNA |
| 2 | 2385 | 100.0 | 1924 | 9 HSLPLR X14390 Human mRNA |
| 3 | 2385 | 100.0 | 2385 | 9 AK092286 AK092286 Homo sapi |
| 4 | 2385 | 100.0 | 3549 | 6 CQ785974 CQ785974 Sequence |

| RESULT 1 | | ALIGNMENTS | |
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| DEFINITION | Human mRNA for lipoprotein lipase | DEFINITION | Human mRNA for lipoprotein lipase (EC 3.1.1.34). |
| ACCESSION | X54516 | ACCESSION | X54516 |
| VERSION | X54516.1 | VERSION | GI:34382 |
| KEYWORDS | Lipase; lipoprotein lipase. | KEYWORDS | Lipase; lipoprotein lipase. |
| SOURCE | Homo sapiens (human) | SOURCE | Homo sapiens (human) |
| ORGANISM | Homo sapiens | ORGANISM | Homo sapiens |
| REFERENCE | 1 (bases 1 to 1612) | REFERENCE | 1 (bases 1 to 1612) |
| AUTHORS | Takagi, A., Ikeda, Y. and Yamamoto, A. | AUTHORS | Takagi, A., Ikeda, Y. and Yamamoto, A. |
| TITLE | DNA sequence of lipoprotein lipase cDNA cloned from human monocytic leukemia THP-1 cells | TITLE | DNA sequence of lipoprotein lipase cDNA cloned from human monocytic leukemia THP-1 cells |
| JOURNAL | Nucleic Acids Res. 18 (21), 6436 (1990) | JOURNAL | Nucleic Acids Res. 18 (21), 6436 (1990) |
| MEDLINE | 91057142 | MEDLINE | 91057142 |
| PubMed | 2243796 | PubMed | 2243796 |
| REFERENCE | 2 (bases 1 to 1612) | REFERENCE | 2 (bases 1 to 1612) |
| AUTHORS | Takagi, A. | AUTHORS | Takagi, A. |
| TITLE | Direct Submission | TITLE | Direct Submission |
| JOURNAL | Submitted (28-AUG-1990) Takagi A., National Cardiovascular Center Research Institute, Dept of Etiology and Pathophysiology, 5-7-1 Fujihiroda, Suita, Osaka 565, Japan | JOURNAL | Submitted (28-AUG-1990) Takagi A., National Cardiovascular Center Research Institute, Dept of Etiology and Pathophysiology, 5-7-1 Fujihiroda, Suita, Osaka 565, Japan |
| COMMENT | Data kindly reviewed (04-DEC-1990) by Takagi A. | COMMENT | Data kindly reviewed (04-DEC-1990) by Takagi A. |
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| 11 | 2380 | 99.8 | 1428 | 12 | BT008284 | Synthetic |
| 12 | 2380 | 99.8 | 1428 | 9 | BC011353 | Homo sapi |
| 13 | 2371 | 99.4 | 1428 | 9 | CR457054 | Homo sapi |
| 14 | 2368 | 99.3 | 3433 | 9 | AF403770 | Macaca fa |
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| C 16 | 2305 | 96.6 | 3544 | 11 | BV180478 | Mustela v |
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| 18 | 2275 | 95.4 | 1511 | 4 | FCU42725 | Felis catus |
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| 34 | 1578 | 66.2 | 1904 | 5 | BC064296 | Danio rer |
| 35 | 1538 | 64.5 | 1982 | 5 | AF358669 | Oncorhync |
| 36 | 1538 | 64.5 | 2022 | 5 | OMAJ4693 | Oncorhync |
| 37 | 1370.5 | 57.5 | 2946 | 5 | AB054062 | Pagrus ma |
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ORIGIN

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-019-341-3 (1-448) x HSLIPAS (1-1612)

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VERSION X14390.1 GI:34404
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1924)
AUTHORS Gotoda,T., Senda,M., Gamou,T., Furuichi,Y. and Oka,K.
Nucleotide sequence of human cDNA coding for a lipoprotein lipase
(LPL) cloned from placental cDNA library
JOURNAL Nucleic Acids Res. 17 (6), 2351 (1989)
MEDLINE 89202044

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PUBMED 2701938
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 AUTHORS Senda, M.
 TITLE Direct Submission
 JOURNAL Nippon Roche Research Center, 200 Kaziwara Kamakura shi, Kanagawa 247, Japan
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 Score: 2385.00 Matches: 448
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US-10-019-341-3 (1-448) x HSLPLR (1-1924)

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RESULT 3

AK092286

LOCUS

DEFINITION

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Mon Oct 25 15:42:52 2004

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to LIPOPROTEIN LIPASE PRECURSOR (EC 3.1.1.34).

AK092286 1 GI:21750843

oligo capping; fis (full insert sequence).

o Homo sapiens (human)

o Homo sapiens

o Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

o Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,

Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H.,

Sekine, M., Obara, Y., Miki, T., Shibahara, T., Tanaka, T.,

Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y.,

Negahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M.,

Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,

Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T.,

Kikkawa, E., Omura, Y., Abe, K., Kamiyama, K., Katsura, N., Sato, K.,

Yamamoto, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H.,

Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M.,

Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S.,

Yosida, M., Hotate, T., Kusano, J., Kanehori, K., Takahashi, F.,

Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R.,

Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A.,

Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T.,

Shiohata, N., Sano, S., Mori, S., Momiya, H., Sato, N., Takami, S.,

Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H.,

Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T.,

Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K.,

Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M.,

Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y.,

Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hiki, J., Kobatake, N.,

Inagaki, H., Ikema, Y., Okamoto, S., Senba, T., Matsumura, K.,

Noguchi, S., Ttoh, T., Shigeta, K., Senba, T., Matsumura, K.,

Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T.,

Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J.,

Sato, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K.,

Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R.,

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Complete sequencing and characterization of 21,243 full-length

human cDNAs

Nat. Genet. 36 (1), 40-45 (2004)

14702039

2

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Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M.,

Sugiyama, T., Irie, K., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,

Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,

Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,

Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,

Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,

Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.

NEDO human cDNA sequencing project

Unpublished

3 (bases 1 to 2385)

Isogai, T. and Yamamoto, J.

Direct Submission

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatac, Kisarazu, Chiba 292-0812, Japan

(E-mail: genomics@kic.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5' - & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

ORIGIN

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Conservative: 0

Mismatches: 0

Best Local Similarity: 100.00%

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Qy

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Qy

41 HisPheAsnHisSerSerLysThrPheMetValLeuHisGlyTyrThrValThrGlyMet 60

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Qy

61 TyrGluSerTyrValProLysLeuValAlaLeuTyrLysArgGluProAspSerAsn 80

408 TATGAGAGTTGGTGCCAAACTTGTGGCCGCTGTACGAGAGAACCCAGACTCCAAT 467

Qy

81 ValLeuValValAspTyrLysSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100

468 GTCAATGTGTGGACTGTGTGCAGGCTCAGGAGCATTTACCCAGTGTCCGCGGCTAC 527

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528 ACCAACTGGTGGGACAGGATGTGGCCCGCTTATCACTGGTGGAGGAGGATTTAAC 587

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588 TACCTCTGGCAATGTCCATCTCTTGGGATATACAGCTTGGAGCCCATTTGCTGTCATT 647

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161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAlaAspPheValAsp 180

708 AACCTTTGAGTATGCAGAACCCCGAGTGTCTTCTCTCTGATGATGAGATTTGTAGAC 767

Qy

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768 GTCTTACACATTTCCAGAGGCTCCCTGTGTGAGAGCATTTGGAATCCAGAAACCACTT 827

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828 GGGCAUUTTGACATTTTACCCGAGTGGAGTACTTTTCAGCCAGGATGTAAATTTGGAGAA 887

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1008 GCCTACAGTGCAGTTCACAGGACCTTTGAGAAAGGCTCTGCTGAGTTGTAGAAG 1067

Qy

281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerLys 300

REFERENCE

1

Isogai, T. and Yamamoto, J.

Direct Submission

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatac, Kisarazu, Chiba 292-0812, Japan

(E-mail: genomics@kic.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5' - & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.

Location/Qualifiers

1..2385

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

FEATURES

source


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Db      1128 ATGTACCTGAAGACTCGTTCTCAGATGCCCTACAAAGCTCTCCATTACCAAGTAAAGATT 1187
Qy      321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
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RESULT 4
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

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Sequence 15 from Patent EP1398032.
CO785974.1 GI:45721151
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kober, I., Albers, M., Koegl, M., Blume, B., Deuschle, U. and
Kremoser, C.
4-Oxo-quinazolines as LXR nuclear receptor binding compounds
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Phenex Pharmaceuticals AG (DE)
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Qy      81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
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us-10-019-341-3.rge

Mon Oct 25 15:42:52 2004

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| DB | 676 | GCAGGAAGTCTGACCAATAAGAAAGTCAACAGAAATTTACTGGCTTCGATCCAGCTGGACCT | 735 | | |
| QY | 161 | AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp | 180 | | |
| DB | 736 | AACTTTGAGTATGACAGAGCCCGAGTCTCTTCTCTGATGATGACAGATTTTGTAGAC | 795 | | |
| QY | 181 | ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal | 200 | | |
| DB | 796 | GTCTTACACACATTCACAGAGGTCCTCTGGTGAAGCATTTGGAAATCCAGAACCCAGTT | 855 | | |
| QY | 201 | GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu | 220 | | |
| DB | 856 | GGGCATGTTGACATTTACCCGAATGGAGTACTTTTCAGCCAGGATCTTAACATTTGGAGAA | 915 | | |
| QY | 221 | AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer | 240 | | |
| DB | 916 | GCTATCCGCGTATTGACAGAGAGAGGACTTGGAGATGTGCACAGCTAGTAGAAGTGTCTCC | 975 | | |
| QY | 241 | HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys | 260 | | |
| DB | 976 | CACGAGCGCTCCATTCATCTCTTCATCGACTCTCTGTTGAATGAAGAAATCCAAAGTAAG | 1035 | | |
| QY | 261 | AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys | 280 | | |
| DB | 1036 | GCCTACAGGTGCGATTTCCAGAGAGCCCTTTCAGAAAAGGCTCTGCTTGAGTTGTAGAAG | 1095 | | |
| QY | 281 | AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys | 300 | | |
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| QY | 321 | HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr | 340 | | |
| DB | 1216 | CATTTTCTGGGACTGAGAGTGAACCCATACCAATCAGGCCCTTTGAGATTTCTCTGTAT | 1275 | | |
| QY | 341 | GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys | 360 | | |
| DB | 1276 | GGCACCGTGGCCGAGAGTGAAGAACATCCCATTCCTCTGCTGAAGTTTCCACAAATAAG | 1335 | | |
| QY | 361 | ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeu | 380 | | |
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| QY | 381 | LysTrpLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerSerProGlyPheAla | 400 | | |
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| QY | 401 | IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg | 420 | | |
| DB | 1456 | ATTGAGAAATCAGAGTAAAGCAGGAGAGACTCAGAAAAGGTGATCTCTCTCTCTAGG | 1515 | | |
| QY | 421 | GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp | 440 | | |
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| RESULT 6 | AX334735 | 3549 bp | DNA | linear | PAT 09-JAN-2002 |
| LOCUS | AX334735 | Sequence 5244 from Patent WO0194629. | | | |
| DEFINITION | AX334735 | | | | |
| ACCESSION | AX334735.1 | GI:18125454 | | | |
| VERSION | AX334735.1 | GI:18125454 | | | |
| KEYWORDS | | | | | |
| SOURCE | Homo sapiens (human) | | | | |
| ORGANISM | Homo sapiens | | | | |

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|---|---|--|------|--------|-----------------|
| DB | 1396 | AAATGGAAGAGTGAATTCATCTTTAGCTGGTGGAGCAGCTCCCGGCTTCGCC | 1455 | | |
| QY | 401 | IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg | 420 | | |
| DB | 1456 | ATTCAGAGATCAGAGTAAAGCAGGAGAGACTCAGAAAAGGTGATCTTCTGTTCTAGG | 1515 | | |
| QY | 421 | GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp | 440 | | |
| DB | 1516 | GAGAAAGTGTCTCATTTGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG | 1575 | | |
| QY | 441 | LysSerLeuAsnLysLysSerGly | 448 | | |
| DB | 1576 | AAGTCTCTGAATAAGAGTCCAGGC | 1599 | | |
| RESULT 5 | AR474623 | 3549 bp | DNA | linear | PAT 20-FEB-2004 |
| LOCUS | AR474623 | Sequence 39 from patent US 6692909. | | | |
| DEFINITION | AR474623 | | | | |
| ACCESSION | AR474623 | | | | |
| VERSION | AR474623.1 | GI:42713737 | | | |
| KEYWORDS | | | | | |
| SOURCE | Unknown. | | | | |
| ORGANISM | Unknown. | | | | |
| REFERENCE | 1 (bases 1 to 3549) | | | | |
| AUTHORS | Lander, E.S., Daley, G.O., Cargill, M., Ireland, J.S. and Rozen, S.G. | | | | |
| TITLE | Coding sequence polymorphisms in vascular pathology genes | | | | |
| JOURNAL | Patent: US 6692909-A 39 17-FEB-2004; | | | | |
| FEATURES | Location/Qualifiers | | | | |
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| Percent Similarity: | 100.00% | Conservative: | 0 | | |
| Best Local Similarity: | 100.00% | Mismatches: | 0 | | |
| Query Match: | 100.00% | Indels: | 0 | | |
| DB: | 6 | Gaps: | 0 | | |
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| QY | 21 | AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys | 40 | | |
| DB | 316 | GACACAGCTGAGGACACTTGCACCTCATTCGCCGAGTAGCAGAGTCCGTGGCTACCTGT | 375 | | |
| QY | 41 | HisPheAsnHisSerSerLysThrPheMetValIleHisGlyThrThrValThrGlyMet | 60 | | |
| DB | 376 | CATTTCATCATCAGCAGCAAAACCTTCATGCTGATCCATGCTGCGAGGTAAACAGGAATG | 435 | | |
| QY | 61 | TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn | 80 | | |
| DB | 436 | TATCAGAGTGGGTGCCAAAACCTTGTGGCCGCCCTGTACAGAGAGAACAGACTCCCAAT | 495 | | |
| QY | 81 | ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr | 100 | | |
| DB | 496 | GTCAATGTGGTGAGCTGGCTGTACCGGCTCAGAGCATTACCCAGTGTCCCGGGCTAC | 555 | | |
| QY | 101 | ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn | 120 | | |
| DB | 556 | ACCAAACTGGTGGCAGGAGATGTGGCCGGTATTATCACTGGATGGAGGAGGAGTTTAA | 615 | | |
| QY | 121 | TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyValAlaHisAlaGlyIle | 140 | | |
| DB | 616 | TACCCTCTGGCAATGTCCATCTCTTGGGATACAGCTTGGAGCCCATCTGCTGGCAT | 675 | | |

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrihan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
gene sets

JOURNAL

Patent: WO 0194629-A 5244 13-DEC-2001;
Avalon Pharmaceuticals (US)

FEATURES

source

1. 3549
Location/Qualifiers
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/mol_type="unassigned DNA"
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ORIGIN

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Pred. No.: 8,456-202 Length: 3549
Score: 2385.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-019-341-3 (1-448) x AX334735 (1-3549)

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DEFINITION MI5856
ACCESSION MI5856
VERSION 1.1 GI:187209
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Wion, K.L., Kirchgessner, T.G., Lusis, A.J., Schotz, M.C. and Lawn, R.M.
Human lipoprotein lipase complementary DNA sequence
Science 235 (4796), 1638-1641 (1987)
87149101
PUBMED 3823907
COMMENT Original source text: Human adipose tissue, cDNA to mRNA, clones
LPL[35,37,46].
Draft entry and clean copy sequence for [1] kindly provided by
R.Lawn, 18-MAY-1987.
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Location/Qualifiers
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| Alignment Scores: | 8.45e-202 | Length: | 3549 |
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| Pred. No.: | 2385.00 | Matches: | 448 |
| Score: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 9 | Gaps: | 0 |

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 Db 256 GCCGACCAAGAAAGAGATTATCGACATCGAAATAAATTTGCCCTAAGGACCCCTGAA 315
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DEFINITION Sequence 5936 from Patent WO02068579.
ACCESSION CQ720002
VERSION CQ720002.1 GI:42280859
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Venter, C. J., Adams, M. C., Li, P. W. and Myers, E. W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 5936 06-SEP-2002;
PE Corporation (NY) (US)
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Best Local Similarity: 100.00% Mismatches: 0
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ACCESSION U18091
VERSION U18091.1 GI:602295
KEYWORDS
SOURCE Papiu anubis (olive baboon)
ORGANISM Papiu anubis
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopitheciinae; Papiu.
1 (bases 1 to 3563)
Cole, S. A. and Hixson, J. E.
Baboon lipoprotein lipase: cDNA sequence and variable
tissue-specific expression of two transcripts
Gene 161 (2), 265-269 (1995)
JOURNAL 95394368
MEDLINE 7665091
PUBMED

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Mon Oct 25 15:42:52 2004

REFERENCE 2 (bases 1 to 3563)
 Cole, S.A.
 Direct Submission
 Submitted (04-DEC-1994) Shelley A. Cole, Genetics, Southwest
 Foundation for Biomedical Research, P.O. Box 28147, San Antonio, TX
 78228-0147, USA

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US-10-019-341-3 (1-448) x PAUL18091 (1-3563)

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 BT006726.1 GI:30582290
 VERSION
 FLI_CDNA
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 ORGANISM
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1428)
 Kainine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
 Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,

Phelan, M. and Farmer, A.
Cloning of human full-length CDSs in BD Creator(TM) System Donor
vector
Unpublished
2 (bases 1 to 1428)
Kalline, N., Chen, X., Rolf, A., Halleck, A., Hines, L., Eisenstein, S.,
Koundinya, M., Raphael, J., Moreira, D., Kelley, T., Labaer, J., Lin, Y.,
Phelan, M. and Farmer, A.
Direct Submission
Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
Circle, Palo Alto, CA 94303, USA
This CDS clone is a part of a collection of human full length
expression clones generated by BD Biosciences Clontech and the
Harvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned using BD In-Fusion(TM)
cloning system between the SalI and HindIII sites of the pDNR-DUAL
vector. Additional sequences in the clone: 'ACC' after SalI site
and before 'ATG' to provide Kozak consensus sequence; 'GG' after
last codon and before HindIII site to maintain reading frame.
Clone distribution: <http://bioinfo.clontech.com/orfclones>.
Location/Qualifiers

| FEATURES | SOURCE |
|--------------------|--------|
| 1. <i>General</i> | |
| 2. <i>Specific</i> | |
| 3. <i>Other</i> | |

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GH00177X1.0"
/clone_lib="BD Creator (TM) CDS Library derived from MGC
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1. 1428
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/protein_id="M4P35372.1"
/db_xref="GI:30582291"
/translation="MESKALLIVLTLAVLWQLSLTASRGGVAAADQRPDIDIESKFAIR
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GAHAAGIAGSLTNKKVNRITGLDPAGNFAYEASRSLSPDDADVDVLHTPTRGSPG
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DLSLNEKPSSKAYRCSKKEAPEKGLCLSCRNRCNVLGYEISKVRKASSSKMYLHKRS
QMPYKVHYQVKIHFSGTESRTHNQAFEISLGYTVAERSENIPTFLPSVTNNTKTYSEL
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ORIGIN

Alignment Scores:

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| Pred. No.: | 7.05e-202 | Length: | 1428 |
| Score: | 2380.00 | Matches: | 447 |
| Percent Similarity: | 100.00% | Conservative: | 1 |
| Best Local Similarity: | 99.78% | Mismatches: | 0 |
| Query Match: | 99.79% | Indels: | 0 |
| DB: | 9 | Gaps: | 0 |

US-10-019-341-3 (1-448) x BT006726 (1-1428)

Qy 1 AlaAspGlnAArgAspPheIleAspIleGluSerLysPheAlaLeuAArgThrProGlu 20
Db 82 GCCGACCAAGAAGAGATTTTATGCATCGAATGTAATTTGCCCTTAAAGACCCCTGA 141

QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
 |||||
 Db 142 GACACAGCTGAGGACACTTGCACCTCATTTCCGGAGTAGCAGATCCGGTGGCTACTCGT 201
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| |
|---|
| OY |
| HisPheAsnHisSerSerLysThrPheMetValIleHISGLYTTrpThrValThrGlyMet 60 |
| |
| Db |
| 202 CATTTCAATCAGCACGAAAAACCTTCATGGTGATCCATGCCTGGACGTACAGAAGT 261 |

| | | | | | | | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|-----|
| Qy | 61 | Tyr | Glu | Ser | Trp | Val | Pro | Lys | Leu | Val | Ala | Ala | Leu | Tyr | Ile | Ser | Arg | Glu | Pro | Ser | Gln | Asn | 80 |
| | | | | | | | | | | | | | | | | | | | | | | | |
| Db | 262 | TAT | GAG | AGT | GGG | TGC | CAAC | ATT | GTG | CGC | CCT | GTG | TAC | AAG | GAG | AGC | ACG | GAC | TCC | CAAT | | | 321 |

| | | | |
|----|------|---|------|
| QY | 81 | ValileValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr | 100 |
| DB | 322 | GTCAATTGTGTGGACTGGCTGTACGGGCTCAGAGCAITACCCAGTGTCCGGGGCTAC | 381 |
| QY | 101 | ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn | 120 |
| DB | 382 | ACCAAACTGGTGGGACAGGATGTGGCCGGTTTATCAACTGGATGGAGGAGGATTTAAAC | 441 |
| QY | 121 | TyrProLeuAspAsnValHisIleuLeuGlyTyrSerLeuGlyAlaHisAlaGlyIle | 140 |
| DB | 442 | TACCTCTGGACAAATGTCATCTCTTGGGATACAGCTTTGGAGCCCATGCTGTGGCAAT | 501 |
| QY | 141 | AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro | 160 |
| DB | 502 | GCAGGAAGTCTGACCAATAAGAAAGTCAACAGAAITACTGGCCTCGATCCAGCTGGACCT | 561 |
| QY | 161 | AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp | 180 |
| DB | 562 | AACITTTGAGTATGCAGAAAGCCCGAGTGGTCTTCTCTCGATGATGCAGATTTTGTAGAC | 621 |
| QY | 181 | ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleInLysProVal | 200 |
| DB | 622 | GTCTTTACACATTCACCAAGAGGGTCCCTGGTGGAGCATTTGGAATCCAGAAACGATTT | 681 |
| QY | 201 | GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu | 220 |
| DB | 682 | GGGCATGTGTGACATTTACCCGAATGGAGTACTTTTCAGCAGGATGTAAACATTTGGAGAA | 741 |
| QY | 221 | AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer | 240 |
| DB | 742 | GCTATCCGCTGATTTGCAGAGAGAGACTTGGAGATGTGGACAGCTAGTGAAGTGCTCC | 801 |
| QY | 241 | HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys | 260 |
| DB | 802 | CACGAGCGCTCCATTCATCTCTCATCGACTCTCTGTGAATGAAGAAATCCCAAGTAAG | 861 |
| QY | 261 | AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys | 280 |
| DB | 862 | GCCTACAGGTGCAGTTCCCAAGGAAGCCTTTGAGAAAGGGCTCTGCTTGAGTTGTAGAAAG | 921 |
| QY | 281 | AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys | 300 |
| DB | 922 | AACCGCTGCAACAATCTGGGCTATGAGATCAGTAAAGTCAGAGCCAAAGACAGACAAA | 981 |
| QY | 301 | MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle | 320 |
| DB | 982 | ATGTACTCGAAGACTCGTTCTCAGATGCCCTACAAAGTCTTCATTTACCAAGTAAAGATT | 1041 |
| QY | 321 | HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr | 340 |
| DB | 1042 | CATTTTCTGGGACTGAGAGTGAACCCCATCAATCAGGCCTTTTGAGATTTCTCTGTAT | 1101 |
| QY | 341 | GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys | 360 |
| DB | 1102 | GGCACCCTGGCCGAGAGTGAGAACATCCCATCTGCTCGCTGAAGTTTCCACAATAG | 1161 |
| QY | 361 | ThrTyrSerPheLeuIleTyrThrGluValAlaPheGlyGluLeuLeuMetLeuLysLeu | 380 |
| DB | 1162 | ACCTACTCTTCTCTAATTTACAGAGGTAGATATTGGAGAACTACTCATGTGAGGCTC | 1221 |
| QY | 381 | LysTrpLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerSerProGlyPheAla | 400 |
| DB | 1222 | AAATGGAAGAGTGTATTCATCTTTAGCTGGTCAGACTGTCGAGCAGCTCCCGGCTTCGC | 1281 |
| QY | 401 | IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg | 420 |
| DB | 1282 | ATTCAGAAAGATCAGAGTAAAGCAGGAGAGACTCAGAAAAAGGTGATCTTCTGTCTTAGG | 1341 |
| QY | 421 | GluLysValSerHisIleuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp | 440 |
| DB | 1342 | GAGAAAGTGTCTCATTTGCAAGAAAGGAAGGCACCTGCGGTATTTGTGAATGCAATGAC | 1401 |
| QY | 441 | LysSerLeuAsnLysLysSerGlyV 448 | |

Mon Oct 25 15:42:52 2004

| | | | | |
|------------------------|------------|----------------------|------|---|
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| DEFINITION | | | | |
| ACCESSION | BT008284 | 1428 bp | mrna | linear SYN 13-MAY-2003 |
| VERSION | BT008284.1 | | | |
| KEYWORDS | FLI CDNA. | | | |
| SOURCE | | | | |
| ORGANISM | | | | |
| REFERENCE | | | | |
| AUTHORS | | | | |
| TITLE | | | | |
| JOURNAL | | | | |
| REFERENCE | | | | |
| AUTHORS | | | | |
| COMMENT | | | | |
| TITLE | | | | |
| JOURNAL | | | | |
| FEATURES | | | | |
| source | | | | |
| CDs | | | | |
| ORIGIN | | | | |
| Alignment Scores: | | | | |
| Pred. No.: | 7,05e-202 | Length: | 1428 | |
| Score: | 2380.00 | Matches: | 447 | |
| Percent Similarity: | 100.00% | Conservative: | 1 | |
| Best local Similarity: | 99.78% | Mismatches: | 0 | |
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Db 1463 AAGTCTCTGATGAAGAAGTCAGGC 1486

RESULT 13

CR457054

LOCUS

DEFINITION

SOURCE

ACCESSION

VERSION

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

383 GTCATTGTGGTGGCTGCTGTCACGGCTCAGGACATTACCCAGTGTCCGGGCTAC 442
 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120
 443 ACCAAACTGGTGGGACAGATGTGGCCGGTATTCACTGGATGGAGGAGGAGTTTAAAC 502
 121 TyrProIleuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaGlyIle 140
 503 TACCCTCTGGACATGTCACATCTCTTGGGATACAGCTTGGAGCCCATGCTGGCATT 562
 141 AlaGlySerLeuThrAsnLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
 563 GCAGGAAGTCTGACCATAGAAAGTCAACAGAAATTACTGGCTCGATCCAGCTGGACCT 622
 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
 623 AACTTTGAGTATGCAGAGCCCGAGTGGTCTTCTCTGATGATGAGATTTGTAGAC 682
 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
 683 GTCTTACACATTCACAGAGGTCCCTGCTGGAAGATTGGAATCCAGAAACCAAGTT 742
 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
 743 GGGCATGTTGACATTTACCCGAATGGAGGTACTTTTCAGCCAGGATGTAAATCCAGAA 802
 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
 803 GCTATCCGCGTATTCAGAGAGAGGATTTGAGATGTGGACCATGAGTGTAGTCTCC 862
 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
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 381 LysTrpLysSerAspSerTyrPheSerTyrSerAspTrpTrpSerSerProGlyPheAla 400
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 1343 ATTACAGAGATTCAGATTAAGACAGAGAGACTCAGAAAGAGTGTATCTTCTGTTCTAGG 1402
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 441 LysSerLeuAsnLysLysSerGly 448

CR457054 1428 bp mRNA linear PRI 03-JUN-2004
 Homo sapiens full open reading frame cDNA clone RZPD0834C0418D for
 gene LPL, lipoprotein lipase; complete cds, incl. stopcodon.

CR457054 1 GI:48146224
 CR457054.1 Full ORF shuttle clone, Gateway(TM), complete cds.
 Homo sapiens (human)

CR457054.1 GI:48146224
 Full ORF shuttle clone, Gateway(TM), complete cds.
 Homo sapiens (human)

CR457054.1 GI:48146224
 Full ORF shuttle clone, Gateway(TM), complete cds.
 Homo sapiens (human)

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 Full ORF shuttle clone, Gateway(TM), complete cds.
 Homo sapiens (human)

CR457054.1 GI:48146224
 Full ORF shuttle clone, Gateway(TM), complete cds.
 Homo sapiens (human)

CR457054.1 GI:48146224
 Full ORF shuttle clone, Gateway(TM), complete cds.
 Homo sapiens (human)

FEATURES

source

1. 1428

/organism="Homo sapiens"

/mol_type="mRNA"

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/lab_host="DH10B"

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1. 1428

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1. 1428

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/protein_id="CAG33335.1"

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gene

CDS

RSTGIQKPVGHVDIYPNGGTFOFGNIGEAIVIAERGLGDVDQIVKCSHERFTHLPT
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ORIGIN

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| Pred. No.: | 4.45e-201 | Length: | 1428 |
| Score: | 2371.00 | Matches: | 446 |
| Percent Similarity: | 99.55% | Conservative: | 0 |
| Best Local Similarity: | 99.55% | Mismatches: | 2 |
| Query Match: | 99.41% | Indels: | 0 |
| DB: | 9 | Gaps: | 0 |

US-10-019-341-3 (1-448) x CR457054 (1-1428)

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| Db | 82 | GGCGACCAAGAGAGAGATTTTATCGACATCGAAAGTAAATTTGCCTCTAAGAGCCCTGAA | 141 |
| QY | 21 | AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys | 40 |
| Db | 142 | GACACAGCTGAGGACACTTGCACCTATTCCCGAGTACGAGATCCGTGGCTACTCTGT | 201 |
| QY | 41 | HisPheAsnHisSerSerIysThrPheMetValIleHisGlyTrpThrValThrGlyMet | 60 |
| Db | 202 | CATTTCATCATCAGCAGCAAAACCTTCATGGTGATCCATGGCTGGACGGTAACAGGAATG | 261 |
| QY | 61 | TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrIysArgGluProAspSerAsn | 80 |
| Db | 262 | TATCAGAGTTGGGTGTCAAACCTTGTGGCCGCCCTGTACAAGAGAGAACACAGATCCAAAT | 321 |
| QY | 81 | ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr | 100 |
| Db | 322 | GTCAATTGTGTGGACTGGCTGTCACTGGCTCAGAGCATTTCCAGTGTCCGGGGCTAC | 381 |
| QY | 101 | ThrIysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluPheAsn | 120 |
| Db | 382 | ACCAAACTGTGGAGCAGGATGTGGCCCGGTTTATCACTGATGAGGAGGAGTTTAAAC | 441 |
| QY | 121 | TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyValAlaHisAlaGlyIle | 140 |
| Db | 442 | TACCCCTCTGGACAAATGTCATCTCTTGGGATACAGCCTTGGAGGCCATGCTGTGGCATT | 501 |
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| Db | 502 | GCAGGAAGTCTGCACCAATAAGAAAGTCAACAGAAATTACTGGCTCGATCGAGTGGACCT | 561 |
| QY | 161 | AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValasp | 180 |
| Db | 562 | AACTTTGATGTACGAAAGCCCGAGTGGCTCTTCTCTGATGATGACGATTTTGTAGAC | 621 |
| QY | 181 | ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal | 200 |
| Db | 622 | GTCTTACACACATTCCACAGAGGTCCTCGTGTGAGCATTTGAAATCCAGAAACCAAGTT | 681 |
| QY | 201 | GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu | 220 |
| Db | 682 | GGGCGATGTTCATTTACCGAATGAGGTTACTTTTCAGCCAGGATGTACATTGGAGAA | 741 |
| QY | 221 | AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer | 240 |
| Db | 742 | GCTATCCCGGTGATTTCAGAGAGAGGACTTGGAGATGTGGACCAAGCTAGTGAAGTCTCC | 801 |
| QY | 241 | HisGluArgSerIleHisLeuPheIleAspSerLeuAsnGlnGluAsnProSerLys | 260 |
| Db | 802 | CACGAGCGCTTCATTCATCTCTTCATCGACTCTCTGTGTAATGAAGAAATCCAGTAAG | 861 |
| QY | 261 | AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysValLeuSerCysArgLys | 280 |
| Db | 862 | GCCTACAGGTCAAGTTCACAGGAAGCCTTTGAGNAAGGGCTCTGCTGTAGTTTGAAG | 921 |

| | | | |
|----|------|---|------|
| Qy | 281 | AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerLys | 300 |
| Db | 922 | AACCGCTGCAACAATCTGGGCTATGAGATCAATTAAGTCAGAGCCAAAGAAGCAGCAAA | 981 |
| Qy | 301 | MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle | 320 |
| Db | 982 | ATGTACCTGAAGACTCGTTCTCAGATGCCCTACAAGTCCTCCATTACCAAGTAAGAAATT | 1041 |
| Qy | 321 | HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr | 340 |
| Db | 1042 | CAITTTTCTGGGACTGAGAGTGAAACCATACCAATCAGGCCITTGAGATTTCTCTGTAT | 1101 |
| Qy | 341 | GlyThrValAlaGluSerGluAsnIleProPheThrIleuProGluValSerThrAsnLys | 360 |
| Db | 1102 | GGCACCGTGGCCGAGAGTGAGAAATCCCATTCACCTGCGCTGAAGTTTCCACAAATAAG | 1161 |
| Qy | 361 | ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeu | 380 |
| Db | 1162 | ACCTACTCTCTCTAATTTACACAGAGGTAGATATTGGAGAACTACTCATGTTGGAAGCTC | 1221 |
| Qy | 381 | LysTrpLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerProGlyPheAla | 400 |
| Db | 1222 | AAATGAAGAGTGATTCACTACTTTAGCTGGTCAGACTGTGGAGCAGTCCCGGCTTCGCC | 1281 |
| Qy | 401 | IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg | 420 |
| Db | 1282 | ATTCAGAGATCAGAGTAAACAGAGAGAGACTCAGAAAAGAGTGATCTCTTGTTCTAGG | 1341 |
| Qy | 421 | GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp | 440 |
| Db | 1342 | GAGAAAGTGTTCTCAITTCGAGAAAGGAAGGCACCTGCGGTATTGTGAAATGCCATGAC | 1401 |
| Qy | 441 | LysSerLeuAsnLysLysSerGly | 448 |
| Db | 1402 | AAGTCTCTGGAATAAGAAGTCAGGT | 1425 |

RESULT 14

AF403770
LOCUS
DEFINITION
AF403770 3433 bp mRNA linear PFI 26-AUG-2001
Macaca fascicularis lipoprotein lipase precursor, mRNA, complete
cde

ACCESSION AF403770

VERSION

KEYWORDS

| | |
|----------|---|
| SOURCE | Macaca fascicularis (crab-eating macaque) |
| ORGANISM | Macaca fascicularis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca. |

REFERENCE

| | |
|----------------|--|
| AUTHORS | Zhou, J., Wilson, K.M. and Medh, J.D. |
| TITLE | Identification of novel peroxisome proliferator activated receptor- γ splice variants and induction of PPAR- γ expression by a high-fat diet in monkey macrophages |
| JOURNAL | Unpublished |

JOURNAL

2 (bases 1 to 3433)
Zhou, J., Wilson, K.M. and Medh, J.D.
Direct Submission
Submitted (26-JUL-2001) Internal Medicine, The University of Iowa,
200 Hawkins Drive, Iowa City IA 52242, USA

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|-----------------|---------------|
| FEATURES | SOURCE |
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PNFESAPRSLSPDADVDVILHFTFRSGPGRSIGLOPKVGHVDIYPNGGTQFQPCN
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LSCRNRCCNLGVEINKVRKSSMYLXTRSDMPYKHYQKIHFSGTSETHNO
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ORIGIN

Alignment Scores: 2.63e-200 Length: 3433
Pred. No.: 2368.00 Matches: 444
Score: 2368.00
Percent Similarity: 100.00% Conservatives: 2
Best Local Similarity: 99.55% Mismatches: 0
Query Match: 99.29% Indels: 0
DB: Gaps: 0

US-10-019-341-3 (1-448) x AF403770 (1-3433)

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| Qy | 3 | GlnArgArgPheIleAspIleGluSerLysPheAlaLeuA-gThrProGluAspThr | 22 |
| Db | 111 | AAAAAGAGAGATTTTATCGACATCGAAGTAAATTTGCCCTAAGACCCCTCGAAGACACA | 170 |
| Qy | 23 | AlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCysHisPhe | 42 |
| Db | 171 | GCTGAGGACATTTGCCACTCATCTCGAGTAGCAGAGTCTGTGGCGACCTGTCACTTC | 230 |
| Qy | 43 | AsnHisSerSerLysPheMetValIleHisGlyThrValThrGlyMetThrGlu | 62 |
| Db | 231 | AATCACAGCAGCAAAACCTTCATGTGTATCCACGGCTGGAGGTAAACAGGAATGTATGAG | 290 |
| Qy | 63 | SerThrValProLysLeuValAlaLeuValLysArgGluProAspSerAsnValIle | 82 |
| Db | 291 | AGTTGGGTGCCAAAACCTTGTGGCTGCTCCCTGTACAGAGAACACGACTCCCAACGTCAAT | 350 |
| Qy | 83 | ValValAspThrLeuSerArgAlaGlnGluHisThrProValSerAlaGlyThrLys | 102 |
| Db | 351 | GTGGTGGAGCTGGCTGTACGGGCTCAGCAGCATTAACAGTGTCCGAGGCTACACCAA | 410 |
| Qy | 103 | LeuValGlyGlnAspValAlaArgPheIleAsnThrMetGluGluPheAsnThrPro | 122 |
| Db | 411 | CTGGTGGGACAGCAGCAGTGGCCGGTTTATCACTGGATGGAGGAGGTTTACTACCT | 470 |
| Qy | 123 | LeuAspAsnValHisLeuLeuGlyThrSerLeuGlyAlaHisAlaAlaGlyIleAlaGly | 142 |
| Db | 471 | CTGCACAAATGCTCATCTCTTGGATACAGCTCGAGCCCATCTGCTGGCATTCGAGGA | 530 |
| Qy | 143 | SerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyProAsnPhe | 162 |
| Db | 531 | AGTCTGACCAATAAGAAAGTCAACAGAAATTAAGTGGCTTGTATCCAGTGGACCTT | 590 |
| Qy | 163 | GluThrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAspValLeu | 182 |
| Db | 591 | GAGTATGCAGAGGCCCGGAGTGGCTTCTCTCTGATGACCGGAGTTTGTAGAGCTCTTA | 650 |
| Qy | 183 | HisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProValGlyHis | 202 |
| Db | 651 | CACACATTCACGAGGTTCCCTGGCCGAGCATTTGAATCCAGAAACCAAGTTGGGCAT | 710 |
| Qy | 203 | ValAspIleThrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGluAlaIle | 222 |
| Db | 711 | GTTCACATTTACCCGATGGAGGTACTTTTCAGCAGGATGATTAATTTGGAGAGCTATT | 770 |
| Qy | 223 | ArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSerHisGlu | 242 |
| Db | 771 | CGCGTGTATGCAGAGAGAGGCTTGGAGATGTGGACCAAGTATGTAAGTGTCCACGAG | 830 |
| Qy | 243 | ArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLysAlaThr | 262 |
| Db | 831 | CGCTCCATTCATCTCTTCATCGACTCCCTGTGTATGAAGAAATTCCAAGTAAGGCCTAC | 890 |
| Qy | 263 | ArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLysAsnArg | 282 |

| | | | |
|----|------|---|------|
| Db | 891 | AGGTGTCAGTCCCAAGAAAGCCCTTTGAGAAAGGGCTCTGCTTGTAGTGTGTAGAAAGACCGC | 950 |
| Qy | 283 | CysAsnAsnLeuGlyThrGluIleAsnLysValArgAlaLysArgSerSerLysMetThr | 302 |
| Db | 951 | TGCAACAATCTGGCTTATGAGATCATAAAGTCAGAGCCAAAGAAAGACGACGATGTAC | 1010 |
| Qy | 303 | LeuLysThrArgSerGlnMetProThrLysValPheHisThrGlnValLysIleHisPhe | 322 |
| Db | 1011 | CTGACAGACTCGTCTTCAGATGCCCTACAAAGTCTTCCATTACCAAGTAAAGATTCAATTT | 1070 |
| Qy | 323 | SerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuThrGlyThr | 342 |
| Db | 1071 | TCTGGGACTCAGAGTGAACCCCATACCAAGCCCTTTGAGATTCTCTGTATGACAC | 1130 |
| Qy | 343 | ValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLysThrThr | 362 |
| Db | 1131 | GTGGCTGAGAGTGAGAAACATCCCATTCACCTGCCTGAGTTTCCACAAATAAGACATAC | 1190 |
| Qy | 363 | SerPheLeuIleThrGluValAspIleGlyGluLeuLeuMetLeuLysLeuLysThr | 382 |
| Db | 1191 | TCCTTCTCTAATTTACACAGAAAGTAGACATTTGGAGACTACTCATGTGAGCTCAATGG | 1250 |
| Qy | 383 | LysSerAspSerThrPheSerThrSerAspThrTrpSerSerProGlyPheAlaIleGln | 402 |
| Db | 1251 | AAGAGCGATTCATCTTCAGCTGGTCAGACTGGTGGAGCAGTCCCGGCTTTGCCATTGAG | 1310 |
| Qy | 403 | LysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArgGluLys | 422 |
| Db | 1311 | AAGATCAGAGTAAAGCCGAGAGACTCAGAAAAAGGTGATCTCTCTGTCTAGGGAGAAA | 1370 |
| Qy | 423 | ValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAspLysSer | 442 |
| Db | 1371 | GTGCTCTACTTGCAGAAAGAAAGGACCTCGGTGATTTGTGAAATGCCATGACAGTCT | 1430 |
| Qy | 443 | LeuAsnLysLysSerGly | 448 |
| Db | 1431 | CTGAATAAGAGTCAGGC | 1448 |

RESULT 15

BV179414/c
LOCUS BV179414.1
DEFINITION sqm105222 Human DNA (Sequence) Homo sapiens STS genomic, sequence tagged site.
ACCESSION BV179414
VERSION BV179414.1
KEYWORDS GI:48016146
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3544)
AUTHORS Nelson, R.M., Marnellos, G., Kammerer, S., Hoyal, C.R., Shi, M.M., Cantor, C.R., and Braun, A.
TITLE Large-Scale Validation of Single Nucleotide Polymorphisms in Gene Regions
JOURNAL Genome Res. (2004) In press
COMMENT Contact: Andreas Braun
Pharmaceuticals division
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 3544.

FEATURES

| | | |
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Search completed: October 24, 2004, 19:58:56
Job time : 6096 secs

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